

60110USPCT1 Corrected SEQ LIST 2-2007.txt
SEQUENCE LISTING



<110> Lanahan, Mike

<120> Self-processing Plants and Plant Parts

<130> 109846.317

<140> PCT/US04/07182

<141> 2004-03-15

<160> 112

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<211> 436

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1

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Gln Lys Ile Pro Glu Trp Tyr Asp Ala Gly Ile Ser Ala Ile Trp Ile
 35      40      45
Pro Pro Ala Ser Lys Gly Met Ser Gly Gly Tyr Ser Met Gly Tyr Asp
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Pro Tyr Asp Tyr Phe Asp Leu Gly Glu Tyr Tyr Gln Lys Gly Thr Val
 65      70      75      80
Glu Thr Arg Phe Gly Ser Lys Gln Glu Leu Ile Asn Met Ile Asn Thr
      85      90      95
Ala His Ala Tyr Gly Ile Lys Val Ile Ala Asp Ile Val Ile Asn His
 100      105      110
Arg Ala Gly Gly Asp Leu Glu Trp Asn Pro Phe Val Gly Asp Tyr Thr
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Trp Thr Asp Phe Ser Lys Val Ala Ser Gly Lys Tyr Thr Ala Asn Tyr
 130      135      140
Leu Asp Phe His Pro Asn Glu Leu His Ala Gly Asp Ser Gly Thr Phe
 145      150      155      160
Gly Gly Tyr Pro Asp Ile Cys His Asp Lys Ser Trp Asp Gln Tyr Trp
      165      170      175
Leu Trp Ala Ser Gln Glu Ser Tyr Ala Ala Tyr Leu Arg Ser Ile Gly
 180      185      190
Ile Asp Ala Trp Arg Phe Asp Tyr Val Lys Gly Tyr Gly Ala Trp Val
 195      200      205
Val Lys Asp Trp Leu Asn Trp Trp Gly Gly Trp Ala Val Gly Glu Tyr
 210      215      220
Trp Asp Thr Asn Val Asp Ala Leu Leu Asn Trp Ala Tyr Ser Ser Gly
 225      230      235      240
Ala Lys Val Phe Asp Phe Pro Leu Tyr Tyr Lys Met Asp Ala Ala Phe
      245      250      255
Asp Asn Lys Asn Ile Pro Ala Leu Val Glu Ala Leu Lys Asn Gly Gly
 260      265      270
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 275      280      285
His Asp Thr Asp Ile Ile Trp Asn Lys Tyr Pro Ala Tyr Ala Phe Ile
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 Trp Leu Asn Lys Asp Lys Leu Lys Asn Leu Ile Trp Ile His Asp Asn
 325 330 335
 Leu Ala Gly Gly Ser Thr Ser Ile Val Tyr Tyr Asp Ser Asp Glu Met
 340 345 350
 Ile Phe Val Arg Asn Gly Tyr Gly Ser Lys Pro Gly Leu Ile Thr Tyr
 355 360 365
 Ile Asn Leu Gly Ser Ser Lys Val Gly Arg Trp Val Tyr Val Pro Lys
 370 375 380
 Phe Ala Gly Ala Cys Ile His Glu Tyr Thr Gly Asn Leu Gly Gly Trp
 385 390 395 400
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Ile	Leu	Gln	Gly	Val	Glu	Glu	Ile	Phe	Tyr	Glu	Lys	Pro	Asp	Thr	Ser
65					70				75					80	
Pro	Arg	Ile	Phe	Phe	Ala	Gln	Ala	Arg	Ser	Asn	Lys	Val	Ile	Glu	Ala
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Phe	Leu	Thr	Asn	Pro	Val	Asp	Thr	Lys	Lys	Lys	Glu	Leu	Phe	Lys	Val
			100					105					110		
Thr	Val	Asp	Gly	Lys	Glu	Ile	Pro	Val	Ser	Arg	Val	Glu	Lys	Ala	Asp
		115					120					125			
Pro	Thr	Asp	Ile	Asp	Val	Thr	Asn	Tyr	Val	Arg	Ile	Val	Leu	Ser	Glu
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				165					170					175	
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Lys	Gly	Asn	Gly	Val	Trp	Glu	Ala	Val	Val	Glu	Gly	Asp	Leu	Asp	Gly
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Val	Phe	Tyr	Leu	Tyr	Gln	Leu	Glu	Asn	Tyr	Gly	Lys	Ile	Arg	Thr	Thr
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Val	Ile	Met	Asp	Met	Val	Phe	Pro	His	Thr	Tyr	Gly	Ile	Gly	Glu	Leu
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Val	Lys	Glu	Tyr	His	Ile	Asp	Gly	Phe	Arg	Phe	Asp	Gln	Met	Gly	Leu
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			500					505					510		
Asp	Pro	Thr	Ile	Ile	Leu	Tyr	Gly	Glu	Pro	Trp	Gly	Gly	Trp	Gly	Ala

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545	Ser	Val	Lys	Gly	Phe	Val	Met	550	Gly	Gly	Tyr	Gly	Lys	555	Glu	Thr	Lys	Ile
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575	Ser	Phe	Ala	Leu	Asp	Pro	Glu	580	Glu	Thr	Ile	Asn	Tyr	585	Ala	Ala	Cys	His
590	Asp	Asn	His	Thr	Leu	Trp	Asp	595	Lys	Asn	Tyr	Leu	Ala	600	Ala	Lys	Ala	Asp
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620	625	Ala	Gly	Ala	Ile	Leu	Leu	630	Thr	Ser	Gln	Gly	Val	635	Pro	Phe	Leu	His
640	645	Gly	Gln	Asp	Phe	Cys	Arg	650	Thr	Thr	Asn	Phe	Asn	655	Asp	Asn	Ser	Tyr
660	665	Ala	Pro	Ile	Ser	Ile	Asn	670	Gly	Phe	Asp	Tyr	Glu	675	Arg	Lys	Leu	Gln
680	685	Ile	Asp	Val	Phe	Asn	Tyr	690	His	Lys	Gly	Leu	Ile	695	Lys	Leu	Arg	Lys
700	705	His	Pro	Ala	Phe	Arg	Leu	710	Lys	Asn	Ala	Glu	Glu	715	Ile	Lys	Lys	His
720	725	Glu	Phe	Leu	Pro	Gly	Arg	730	Arg	Ile	Val	Ala	Phe	735	Met	Leu	Lys	Asp
740	745	His	Ala	Gly	Gly	Asp	Pro	750	Trp	Lys	Asp	Ile	Val	755	Val	Ile	Tyr	Asn
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<211> 693

<212> PRT

<213> Sulfolobus solfataricus

<400> 5

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			20					25					30		
Ser	Ser	Asn	Lys	Ser	Leu	Ser	Glu	Leu	Gly	Leu	Thr	Ile	Val	Gln	Gln
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Ile	Gly	Leu	Gly	Glu	Lys	Ala	Phe	Glu	Leu	Asp	Arg	Lys	Arg	Lys	Arg
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Tyr	Val	Met	Tyr	Asn	Val	Asp	Ala	Gly	Ala	Tyr	Lys	Lys	Tyr	Gln	Asp
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Pro	Leu	Tyr	Val	Ser	Ile	Pro	Leu	Phe	Ile	Ser	Val	Lys	Asp	Gly	Val
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Lys	Tyr	Thr	Glu	Leu	Thr	Gly	Lys	Pro	Phe	Leu	Pro	Pro	Met	Trp	Ala
				165				170						175	
Phe	Gly	Tyr	Met	Ile	Ser	Arg	Tyr	Ser	Tyr	Tyr	Pro	Gln	Asp	Lys	Val
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Val	Phe	Leu	Asp	Ile	His	Tyr	Met	Asp	Ser	Tyr	Lys	Leu	Phe	Thr	Trp
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His	Pro	Tyr	Arg	Phe	Pro	Glu	Pro	Lys	Lys	Leu	Ile	Asp	Glu	Leu	His
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Lys	Arg	Asn	Val	Lys	Leu	Ile	Thr	Ile	Val	Asp	His	Gly	Ile	Arg	Val
				245					250					255	

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 Ile Glu Ser Gly Glu Leu Phe Val Gly Lys Met Trp Pro Gly Thr Thr
 275 280 285
 Val Tyr Pro Asp Phe Phe Arg Glu Asp Thr Arg Glu Trp Trp Ala Gly
 290 295 300
 Leu Ile Ser Glu Trp Leu Ser Gln Gly Val Asp Gly Ile Trp Leu Asp
 305 310 315 320
 Met Asn Glu Pro Thr Asp Phe Ser Arg Ala Ile Glu Ile Arg Asp Val
 325 330 335
 Leu Ser Ser Leu Pro Val Gln Phe Arg Asp Asp Arg Leu Val Thr Thr
 340 345 350
 Phe Pro Asp Asn Val Val His Tyr Leu Arg Gly Lys Arg Val Lys His
 355 360 365
 Glu Lys Val Arg Asn Ala Tyr Pro Leu Tyr Glu Ala Met Ala Thr Phe
 370 375 380
 Lys Gly Phe Arg Thr Ser His Arg Asn Glu Ile Phe Ile Leu Ser Arg
 385 390 395 400
 Ala Gly Tyr Ala Gly Ile Gln Arg Tyr Ala Phe Ile Trp Thr Gly Asp
 405 410 415
 Asn Thr Pro Ser Trp Asp Asp Leu Lys Leu Gln Leu Gln Leu Val Leu
 420 425 430
 Gly Leu Ser Ile Ser Gly Val Pro Phe Val Gly Cys Asp Ile Gly Gly
 435 440 445
 Phe Gln Gly Arg Asn Phe Ala Glu Ile Asp Asn Ser Met Asp Leu Leu
 450 455 460
 Val Lys Tyr Tyr Ala Leu Ala Leu Phe Phe Pro Phe Tyr Arg Ser His
 465 470 475 480
 Lys Ala Thr Asp Gly Ile Asp Thr Glu Pro Val Phe Leu Pro Asp Tyr
 485 490 495
 Tyr Lys Glu Lys Val Lys Glu Ile Val Glu Leu Arg Tyr Lys Phe Leu
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 Pro Tyr Ile Tyr Ser Leu Ala Leu Glu Ala Ser Glu Lys Gly His Pro
 515 520 525
 Val Ile Arg Pro Leu Phe Tyr Glu Phe Gln Asp Asp Asp Met Tyr
 530 535 540
 Arg Ile Glu Asp Glu Tyr Met Val Gly Lys Tyr Leu Leu Tyr Ala Pro
 545 550 555 560
 Ile Val Ser Lys Glu Ser Arg Leu Val Thr Leu Pro Arg Gly Lys
 565 570 575
 Trp Tyr Asn Tyr Trp Asn Gly Glu Ile Ile Asn Gly Lys Ser Val Val
 580 585 590
 Lys Ser Thr His Glu Leu Pro Ile Tyr Leu Arg Glu Gly Ser Ile Ile
 595 600 605
 Pro Leu Glu Gly Asp Glu Leu Ile Val Tyr Gly Glu Thr Ser Phe Lys
 610 615 620
 Arg Tyr Asp Asn Ala Glu Ile Thr Ser Ser Ser Asn Glu Ile Lys Phe
 625 630 635 640
 Ser Arg Glu Ile Tyr Val Ser Lys Leu Thr Ile Thr Ser Glu Lys Pro
 645 650 655
 Val Ser Lys Ile Ile Val Asp Asp Ser Lys Glu Ile Gln Val Glu Lys
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 Thr Met Gln Asn Thr Tyr Val Ala Lys Ile Asn Gln Lys Ile Arg Gly
 675 680 685
 Lys Ile Asn Leu Glu
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<210> 6

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<212> DNA

<213> Sulfolobus solfataricus

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aagtacaccg	agctgaccgg	caagccgttc	ctcccggcca	tgtgggcctt	cggctacatg	540
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tgaacggcg	agatcatcaa	cggaagtcc	gtggtgaagt	ccaccacga	gctgccgatc	1800
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tcccgcgaga	tctacgtgtc	caagctcacc	atcacctccg	agaagccggt	gtccaagatc	1980
atcgtggacg	actccaagga	gatccagggtg	gagaagacca	tgcagaacac	ctacgtggcc	2040
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<210> 7

<211> 1818

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 7

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gcgcgcccgc	gggccagggt	cccgtcgctc	gtcgtgtgcg	ccagcgccgg	catgaacgtc	240
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ggcgccgtgc	cgccggccat	ggccgcgaac	gggcaccgtg	tcatggctgt	ctctccccgc	360
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60110USPCT1 Corrected SEQ LIST 2-2007.txt

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gaggcgctgc aggcggaggt cgggctcccg gtggaccgga acatcccgtt ggtggcggtc 1200
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atggagatgg tggaggacgt gcagatcgtt ctgctgggca cgggcaagaa gaagttcgag 1320
cgcatgctca tgagcgccga ggagaagttc ccaggcaagg tgcgcgccgt ggtcaagttc 1380
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cgcttcagcg tcgactgcaa cgctcgtggag ccggcgggacg tcaagaagggt ggccaccacc 1620
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<210> 8

<211> 606

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 8

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20     25     30
Arg Gly Ala Arg Ala Ser Ala Ala Asp Thr Leu Ser Met Arg Thr
35     40     45
Ser Ala Arg Ala Ala Pro Arg His Gln His Gln Ala Arg Arg Gly
50     55     60
Ala Arg Phe Pro Ser Leu Val Val Cys Ala Ser Ala Gly Met Asn Val
65     70     75     80
Val Phe Val Gly Ala Glu Met Ala Pro Trp Ser Lys Thr Gly Gly Leu
85     90     95
Gly Asp Val Leu Gly Gly Leu Pro Pro Ala Met Ala Ala Asn Gly His
100    105    110
Arg Val Met Val Val Ser Pro Arg Tyr Asp Gln Tyr Lys Asp Ala Trp
115    120    125
Asp Thr Ser Val Val Ser Glu Ile Lys Met Gly Asp Gly Tyr Glu Thr
130    135    140
Val Arg Phe Phe His Cys Tyr Lys Arg Gly Val Asp Arg Val Phe Val
145    150    155    160
Asp His Pro Leu Phe Leu Glu Arg Val Trp Gly Lys Thr Glu Glu Lys
165    170    175
Ile Tyr Gly Pro Val Ala Gly Thr Asp Tyr Arg Asp Asn Gln Leu Arg
180    185    190
Phe Ser Leu Leu Cys Gln Ala Ala Leu Glu Ala Pro Arg Ile Leu Ser
195    200    205
Leu Asn Asn Asn Pro Tyr Phe Ser Gly Pro Tyr Gly Glu Asp Val Val
210    215    220
Phe Val Cys Asn Asp Trp His Thr Gly Pro Leu Ser Cys Tyr Leu Lys
225    230    235    240
Ser Asn Tyr Gln Ser His Gly Ile Tyr Arg Asp Ala Lys Thr Ala Phe
245    250    255
Cys Ile His Asn Ile Ser Tyr Gln Gly Arg Phe Ala Phe Ser Asp Tyr
260    265    270
Pro Glu Leu Asn Leu Pro Glu Arg Phe Lys Ser Ser Phe Asp Phe Ile
275    280    285
Asp Gly Tyr Glu Lys Pro Val Glu Gly Arg Lys Ile Asn Trp Met Lys
290    295    300
Ala Gly Ile Leu Glu Ala Asp Arg Val Leu Thr Val Ser Pro Tyr Tyr

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60110USPCT1 Corrected SEQ LIST 2-2007.txt

305		310		315		320
Ala	Glu	Glu	Leu	Ile	Ser	Gly
Ile	Met	Arg	Leu	Thr	Gly	Ile
Ser	Glu	Trp	Asp	Pro	Ser	Arg
Val	Ser	Thr	Ala	Val	Glu	Ala
Ala	Glu	Val	Gly	Leu	Pro	Val
Ile	Gly	Arg	Leu	Glu	Glu	Gln
Ile	Pro	Gln	Leu	Met	Val	Glu
Gly	Thr	Gly	Lys	Lys	Lys	Phe
Lys	Phe	Pro	Gly	Lys	Val	Arg
Ala	His	His	Ile	Met	Ala	Gly
Phe	Glu	Pro	Cys	Gly	Leu	Ile
Pro	Cys	Ala	Cys	Ala	Ser	Thr
Gly	Lys	Thr	Gly	Phe	His	Met
Val	Glu	Pro	Ala	Asp	Val	Lys
Ile	Lys	Val	Val	Gly	Thr	Pro
Met	Ile	Gln	Asp	Leu	Ser	Trp
Val	Leu	Leu	Ser	Leu	Gly	Val
Glu	Glu	Ile	Ala	Pro	Leu	Ala

<210> 9
 <211> 2223
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 9	
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ggcatcaagg	tcatcgcgga
aaccggttcg	tcggcgacta
accgccaact	acctcgactt
ggcggctacc	cggacatctg
caggagtctt	acgcgcccta
gtcaagggct	acggggcctg
gtgggcgagt	actgggacac
gccaaaggtg	tcgacttccc
atcccggcgc	tcgctcgaggc
aaggccgtga	ccttcgtcgc
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gtgggacacc	atccgccaga
gataccgcca	gcttccaagg
ctacttcgac	ctcggcgagt
atcaacatga	tcaacacggc
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cggcgactc	cggcgactc
agtggtggc	ctgggcctcg
cttcgactac	cttcgactac
cggctggcg	cggctggcg
actgggtggg	cggctggcg
ctcctccggc	ctcctccggc
caacaagaac	caacaagaac
cgacccgttc	cgacccgttc
gtacccggcg	gtacccggcg

60110USPCT1 Corrected SEQ LIST 2-2007.txt

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tccaagcccc gcctgatcac gtacatcaac ctgggctcct ccaagggtgg ccgctgggtg 1140
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tcttggaagg gccctgcca gaactgggag aacgtgctgc tcagcctcgg ggtcgccggc 2160
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<210> 10

<211> 741

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 10

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          20          25          30
Gln Lys Ile Pro Glu Trp Tyr Asp Ala Gly Ile Ser Ala Ile Trp Ile
          35          40          45
Pro Pro Ala Ser Lys Gly Met Ser Gly Gly Tyr Ser Met Gly Tyr Asp
          50          55          60
Pro Tyr Asp Tyr Phe Asp Leu Gly Glu Tyr Tyr Gln Lys Gly Thr Val
65          70          75          80
Glu Thr Arg Phe Gly Ser Lys Gln Glu Leu Ile Asn Met Ile Asn Thr
          85          90          95
Ala His Ala Tyr Gly Ile Lys Val Ile Ala Asp Ile Val Ile Asn His
          100          105          110
Arg Ala Gly Gly Asp Leu Glu Trp Asn Pro Phe Val Gly Asp Tyr Thr
          115          120          125
Trp Thr Asp Phe Ser Lys Val Ala Ser Gly Lys Tyr Thr Ala Asn Tyr
          130          135          140
Leu Asp Phe His Pro Asn Glu Leu His Ala Gly Asp Ser Gly Thr Phe
          145          150          155          160
Gly Gly Tyr Pro Asp Ile Cys His Asp Lys Ser Trp Asp Gln Tyr Trp
          165          170          175
Leu Trp Ala Ser Gln Glu Ser Tyr Ala Tyr Leu Arg Ser Ile Gly
          180          185          190
Ile Asp Ala Trp Arg Phe Asp Tyr Val Lys Gly Tyr Gly Ala Trp Val
          195          200          205
Val Lys Asp Trp Leu Asn Trp Trp Gly Gly Trp Ala Val Gly Glu Tyr
          210          215          220
Trp Asp Thr Asn Val Asp Ala Leu Leu Asn Trp Ala Tyr Ser Ser Gly
          225          230          235          240

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60110USPCT1 Corrected SEQ LIST 2-2007.txt

Ala Lys Val Phe Asp Phe Pro Leu Tyr Tyr Lys Met Asp Ala Ala Phe
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 Asp Asn Lys Asn Ile Pro Ala Leu Val Glu Ala Leu Lys Asn Gly Gly
 260 265 270
 Thr Val Val Ser Arg Asp Pro Phe Lys Ala Val Thr Phe Val Ala Asn
 275 280 285
 His Asp Thr Asp Ile Ile Trp Asn Lys Tyr Pro Ala Tyr Ala Phe Ile
 290 295 300
 Leu Thr Tyr Glu Gly Gln Pro Thr Ile Phe Tyr Arg Asp Tyr Glu Glu
 305 310 315 320
 Trp Leu Asn Lys Asp Lys Leu Lys Asn Leu Ile Trp Ile His Asp Asn
 325 330 335
 Leu Ala Gly Gly Ser Thr Ser Ile Val Tyr Tyr Asp Ser Asp Glu Met
 340 345 350
 Ile Phe Val Arg Asn Gly Tyr Gly Ser Lys Pro Gly Leu Ile Thr Tyr
 355 360 365
 Ile Asn Leu Gly Ser Ser Lys Val Gly Arg Trp Val Tyr Val Pro Lys
 370 375 380
 Phe Ala Gly Ala Cys Ile His Glu Tyr Thr Gly Asn Leu Gly Gly Trp
 385 390 395 400
 Val Asp Lys Tyr Val Tyr Ser Ser Gly Trp Val Tyr Leu Glu Ala Pro
 405 410 415
 Ala Tyr Asp Pro Ala Asn Gly Gln Tyr Gly Tyr Ser Val Trp Ser Tyr
 420 425 430
 Cys Gly Val Gly Thr Ser Ile Ala Gly Ile Leu Glu Ala Asp Arg Val
 435 440 445
 Leu Thr Val Ser Pro Tyr Tyr Ala Glu Glu Leu Ile Ser Gly Ile Ala
 450 455 460
 Arg Gly Cys Glu Leu Asp Asn Ile Met Arg Leu Thr Gly Ile Thr Gly
 465 470 475 480
 Ile Val Asn Gly Met Asp Val Ser Glu Trp Asp Pro Ser Arg Asp Lys
 485 490 495
 Tyr Ile Ala Val Lys Tyr Asp Val Ser Thr Ala Val Glu Ala Lys Ala
 500 505 510
 Leu Asn Lys Glu Ala Leu Gln Ala Glu Val Gly Leu Pro Val Asp Arg
 515 520 525
 Asn Ile Pro Leu Val Ala Phe Ile Gly Arg Leu Glu Glu Gln Lys Gly
 530 535 540
 Pro Asp Val Met Ala Ala Ile Pro Gln Leu Met Glu Met Val Glu
 545 550 555 560
 Asp Val Gln Ile Val Leu Leu Gly Thr Gly Lys Lys Lys Phe Glu Arg
 565 570 575
 Met Leu Met Ser Ala Glu Glu Lys Phe Pro Gly Lys Val Arg Ala Val
 580 585 590
 Val Lys Phe Asn Ala Ala Leu Ala His His Ile Met Ala Gly Ala Asp
 595 600 605
 Val Leu Ala Val Thr Ser Arg Phe Glu Pro Cys Gly Leu Ile Gln Leu
 610 615 620
 Gln Gly Met Arg Tyr Gly Thr Pro Cys Ala Cys Ala Ser Thr Gly Gly
 625 630 635 640
 Leu Val Asp Thr Ile Ile Glu Gly Lys Thr Gly Phe His Met Gly Arg
 645 650 655
 Leu Ser Val Asp Cys Asn Val Val Glu Pro Ala Asp Val Lys Lys Val
 660 665 670
 Ala Thr Thr Leu Gln Arg Ala Ile Lys Val Val Gly Thr Pro Ala Tyr
 675 680 685
 Glu Glu Met Val Arg Asn Cys Met Ile Gln Asp Leu Ser Trp Lys Gly
 690 695 700
 Pro Ala Lys Asn Trp Glu Asn Val Leu Leu Ser Leu Gly Val Ala Gly
 705 710 715 720
 Gly Glu Pro Gly Val Glu Gly Glu Glu Ile Ala Pro Leu Ala Lys Glu
 725 730 735
 Asn Val Ala Ala Pro

740

<210> 11
 <211> 1515
 <212> DNA
 <213> Zea mays

<400> 11
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 cagctcagaa aaaagttatc tatgaaaagg ttcatgtgta ccgtgggaaa tgagaaatgt 180
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 ctctcgtgcc tgtttatittt cttgcccttt ctgatcataa aaaaacatta agagtttgca 480
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 ttcatgggtg ttgatgtctt tacacagttc atctccacca gtatgccctc ctcatactct 960
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 ttttggttac ttgtcttgag gtgcattctt catatgtcca gttttatgga agtaataaac 1380
 ttcagtttgg tcataagatg tcatattaaa gggcaaacat atattcaatg ttcaattcat 1440
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 tagtagttgg aggag 1515

<210> 12
 <211> 673
 <212> DNA
 <213> Zea mays

<400> 12
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 aattgcacgt caaggggtatt gggtaagaaa caatcaaaaca aatcctctct gtgtgcaaa 180
 aaacacgggt agtcatgccg agatcatact catctgatat acatgcttac agctcacaag 240
 acattacaaa caactcatat tgcattacaa agatcgtttc atgaaaaata aaataggccg 300
 gacaggacaa aaatccttga cgtgtaaagt aaatttaca caaaaaaaa gccatatgtc 360
 aagctaaatc taattcgttt tacgtagatc aacaacctgt agaaggcaac aaaactgagc 420
 cacgcagaag tacagaatga ttccagatga accatcgacg tgctacgtaa agagagtga 480
 gagtcatata catttggtgaa gaaacctatga agctgcctac agccgtctcg gtggcataag 540
 aacacaagaa attgtgttaa ttaatcaaa ctataaataa cgctcgcatt cctgtgcact 600
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<210> 13
 <211> 454
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

60110USPCT1 Corrected SEQ LIST 2-2007.txt

<400> 13

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Met Arg Val Leu Leu Val Ala Leu Ala Leu Leu Ala Leu Ala Ala Ser
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20      25      30
Gln Ala Phe Tyr Trp Asp Val Pro Ser Gly Gly Ile Trp Trp Asp Thr
35      40      45
Ile Arg Gln Lys Ile Pro Glu Trp Tyr Asp Ala Gly Ile Ser Ala Ile
50      55      60
Trp Ile Pro Pro Ala Ser Lys Gly Met Ser Gly Gly Tyr Ser Met Gly
65      70      75      80
Tyr Asp Pro Tyr Asp Tyr Phe Asp Leu Gly Glu Tyr Tyr Gln Lys Gly
85      90      95
Thr Val Glu Thr Arg Phe Gly Ser Lys Gln Glu Leu Ile Asn Met Ile
100     105     110
Asn Thr Ala His Ala Tyr Gly Ile Lys Val Ile Ala Asp Ile Val Ile
115     120     125
Asn His Arg Ala Gly Gly Asp Leu Glu Trp Asn Pro Phe Val Gly Asp
130     135     140
Tyr Thr Trp Thr Asp Phe Ser Lys Val Ala Ser Gly Lys Tyr Thr Ala
145     150     155     160
Asn Tyr Leu Asp Phe His Pro Asn Glu Leu His Ala Gly Asp Ser Gly
165     170     175
Thr Phe Gly Gly Tyr Pro Asp Ile Cys His Asp Lys Ser Trp Asp Gln
180     185     190
Tyr Trp Leu Trp Ala Ser Gln Glu Ser Tyr Ala Ala Tyr Leu Arg Ser
195     200     205
Ile Gly Ile Asp Ala Trp Arg Phe Asp Tyr Val Lys Gly Tyr Gly Ala
210     215     220
Trp Val Val Lys Asp Trp Leu Asn Trp Trp Gly Gly Trp Ala Val Gly
225     230     235     240
Glu Tyr Trp Asp Thr Asn Val Asp Ala Leu Leu Asn Trp Ala Tyr Ser
245     250     255
Ser Gly Ala Lys Val Phe Asp Phe Pro Leu Tyr Tyr Lys Met Asp Ala
260     265     270
Ala Phe Asp Asn Lys Asn Ile Pro Ala Leu Val Glu Ala Leu Lys Asn
275     280     285
Gly Gly Thr Val Val Ser Arg Asp Pro Phe Lys Ala Val Thr Phe Val
290     295     300
Ala Asn His Asp Thr Asp Ile Ile Trp Asn Lys Tyr Pro Ala Tyr Ala
305     310     315     320
Phe Ile Leu Thr Tyr Glu Gly Gln Pro Thr Ile Phe Tyr Arg Asp Tyr
325     330     335
Glu Glu Trp Leu Asn Lys Asp Lys Leu Lys Asn Leu Ile Trp Ile His
340     345     350
Asp Asn Leu Ala Gly Gly Ser Thr Ser Ile Val Tyr Tyr Asp Ser Asp
355     360     365
Glu Met Ile Phe Val Arg Asn Gly Tyr Gly Ser Lys Pro Gly Leu Ile
370     375     380
Thr Tyr Ile Asn Leu Gly Ser Ser Lys Val Gly Arg Trp Val Tyr Val
385     390     395     400
Pro Lys Phe Ala Gly Ala Cys Ile His Glu Tyr Thr Gly Asn Leu Gly
405     410     415
Gly Trp Val Asp Lys Tyr Val Tyr Ser Ser Gly Trp Val Tyr Leu Glu
420     425     430
Ala Pro Ala Tyr Asp Pro Ala Asn Gly Gln Tyr Gly Tyr Val Trp
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Ser Tyr Cys Gly Val Gly
450

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<210> 14

<211> 460

60110USPCT1 Corrected SEQ LIST 2-2007.txt

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 14

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Met Arg Val Leu Leu Val Ala Leu Ala Leu Leu Ala Leu Ala Ala Ser
 1      5      10      15
Ala Thr Ser Ala Lys Tyr Leu Glu Leu Glu Glu Gly Gly Val Ile Met
 20      25      30
Gln Ala Phe Tyr Trp Asp Val Pro Ser Gly Gly Ile Trp Trp Asp Thr
 35      40      45
Ile Arg Gln Lys Ile Pro Glu Trp Tyr Asp Ala Gly Ile Ser Ala Ile
 50      55      60
Trp Ile Pro Pro Ala Ser Lys Gly Met Ser Gly Gly Tyr Ser Met Gly
 65      70      75      80
Tyr Asp Pro Tyr Asp Tyr Phe Asp Leu Gly Glu Tyr Tyr Gln Lys Gly
 85      90      95
Thr Val Glu Thr Arg Phe Gly Ser Lys Gln Glu Leu Ile Asn Met Ile
100      105      110
Asn Thr Ala His Ala Tyr Gly Ile Lys Val Ile Ala Asp Ile Val Ile
115      120      125
Asn His Arg Ala Gly Gly Asp Leu Glu Trp Asn Pro Phe Val Gly Asp
130      135      140
Tyr Thr Trp Thr Asp Phe Ser Lys Val Ala Ser Gly Lys Tyr Thr Ala
145      150      155      160
Asn Tyr Leu Asp Phe His Pro Asn Glu Leu His Ala Gly Asp Ser Gly
165      170      175
Thr Phe Gly Gly Tyr Pro Asp Ile Cys His Asp Lys Ser Trp Asp Gln
180      185      190
Tyr Trp Leu Trp Ala Ser Gln Glu Ser Tyr Ala Ala Tyr Leu Arg Ser
195      200      205
Ile Gly Ile Asp Ala Trp Arg Phe Asp Tyr Val Lys Gly Tyr Gly Ala
210      215      220
Trp Val Val Lys Asp Trp Leu Asn Trp Trp Gly Gly Trp Ala Val Gly
225      230      235      240
Glu Tyr Trp Asp Thr Asn Val Asp Ala Leu Leu Asn Trp Ala Tyr Ser
245      250      255
Ser Gly Ala Lys Val Phe Asp Phe Pro Leu Tyr Tyr Lys Met Asp Ala
260      265      270
Ala Phe Asp Asn Lys Asn Ile Pro Ala Leu Val Glu Ala Leu Lys Asn
275      280      285
Gly Gly Thr Val Val Ser Arg Asp Pro Phe Lys Ala Val Thr Phe Val
290      295      300
Ala Asn His Asp Thr Asp Ile Ile Trp Asn Lys Tyr Pro Ala Tyr Ala
305      310      315      320
Phe Ile Leu Thr Tyr Glu Gly Gln Pro Thr Ile Phe Tyr Arg Asp Tyr
325      330      335
Glu Glu Trp Leu Asn Lys Asp Lys Leu Lys Asn Leu Ile Trp Ile His
340      345      350
Asp Asn Leu Ala Gly Gly Ser Thr Ser Ile Val Tyr Tyr Asp Ser Asp
355      360      365
Glu Met Ile Phe Val Arg Asn Gly Tyr Gly Ser Lys Pro Gly Leu Ile
370      375      380
Thr Tyr Ile Asn Leu Gly Ser Ser Lys Val Gly Arg Trp Val Tyr Val
385      390      395      400
Pro Lys Phe Ala Gly Ala Cys Ile His Glu Tyr Thr Gly Asn Leu Gly
405      410      415
Gly Trp Val Asp Lys Tyr Val Tyr Ser Ser Gly Trp Val Tyr Leu Glu
420      425      430
Ala Pro Ala Tyr Asp Pro Ala Asn Gly Gln Tyr Gly Tyr Val Trp
435      440      445

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Ser Tyr Cys Gly Val Gly Ser Glu Lys Asp Glu Leu
 450 455 460

<210> 15
 <211> 518
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 15
 Met Leu Ala Ala Leu Ala Thr Ser Gln Leu Val Ala Thr Arg Ala Gly
 1 5 10 15
 Leu Gly Val Pro Asp Ala Ser Thr Phe Arg Arg Gly Ala Ala Gln Gly
 20 25 30
 Leu Arg Gly Ala Arg Ala Ser Ala Ala Asp Thr Leu Ser Met Arg
 35 40 45
 Thr Ser Ala Arg Ala Ala Pro Arg His Gln His Gln Ala Arg Arg
 50 55 60
 Gly Ala Arg Phe Pro Ser Leu Val Val Cys Ala Ser Ala Gly Ala Met
 65 70 75 80
 Ala Lys Tyr Leu Glu Leu Glu Glu Gly Gly Val Ile Met Gln Ala Phe
 85 90 95
 Tyr Trp Asp Val Pro Ser Gly Gly Ile Trp Trp Asp Thr Ile Arg Gln
 100 105 110
 Lys Ile Pro Glu Trp Tyr Asp Ala Gly Ile Ser Ala Ile Trp Ile Pro
 115 120 125
 Pro Ala Ser Lys Gly Met Ser Gly Gly Tyr Ser Met Gly Tyr Asp Pro
 130 135 140
 Tyr Asp Tyr Phe Asp Leu Gly Glu Tyr Tyr Gln Lys Gly Thr Val Glu
 145 150 155 160
 Thr Arg Phe Gly Ser Lys Gln Glu Leu Ile Asn Met Ile Asn Thr Ala
 165 170 175
 His Ala Tyr Gly Ile Lys Val Ile Ala Asp Ile Val Ile Asn His Arg
 180 185 190
 Ala Gly Gly Asp Leu Glu Trp Asn Pro Phe Val Gly Asp Tyr Thr Trp
 195 200 205
 Thr Asp Phe Ser Lys Val Ala Ser Gly Lys Tyr Thr Ala Asn Tyr Leu
 210 215 220
 Asp Phe His Pro Asn Glu Leu His Ala Gly Asp Ser Gly Thr Phe Gly
 225 230 235 240
 Gly Tyr Pro Asp Ile Cys His Asp Lys Ser Trp Asp Gln Tyr Trp Leu
 245 250 255
 Trp Ala Ser Gln Glu Ser Tyr Ala Ala Tyr Leu Arg Ser Ile Gly Ile
 260 265 270
 Asp Ala Trp Arg Phe Asp Tyr Val Lys Gly Tyr Gly Ala Trp Val Val
 275 280 285
 Lys Asp Trp Leu Asn Trp Trp Gly Gly Trp Ala Val Gly Glu Tyr Trp
 290 295 300
 Asp Thr Asn Val Asp Ala Leu Leu Asn Trp Ala Tyr Ser Ser Gly Ala
 305 310 315 320
 Lys Val Phe Asp Phe Pro Leu Tyr Tyr Lys Met Asp Ala Ala Phe Asp
 325 330 335
 Asn Lys Asn Ile Pro Ala Leu Val Glu Ala Leu Lys Asn Gly Gly Thr
 340 345 350
 Val Val Ser Arg Asp Pro Phe Lys Ala Val Thr Phe Val Ala Asn His
 355 360 365
 Asp Thr Asp Ile Ile Trp Asn Lys Tyr Pro Ala Tyr Ala Phe Ile Leu
 370 375 380
 Thr Tyr Glu Gly Gln Pro Thr Ile Phe Tyr Arg Asp Tyr Glu Glu Trp
 385 390 395 400

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Leu Asn Lys Asp Lys Leu Lys Asn Leu Ile Trp Ile His Asp Asn Leu
 405 410 415
 Ala Gly Gly Ser Thr Ser Ile Val Tyr Tyr Asp Ser Asp Glu Met Ile
 420 425 430
 Phe Val Arg Asn Gly Tyr Gly Ser Lys Pro Gly Leu Ile Thr Tyr Ile
 435 440 445
 Asn Leu Gly Ser Ser Lys Val Gly Arg Trp Val Tyr Val Pro Lys Phe
 450 455 460
 Ala Gly Ala Cys Ile His Glu Tyr Thr Gly Asn Leu Gly Gly Trp Val
 465 470 475 480
 Asp Lys Tyr Val Tyr Ser Ser Gly Trp Val Tyr Leu Glu Ala Pro Ala
 485 490 495
 Tyr Asp Pro Ala Asn Gly Gln Tyr Gly Tyr Ser Val Trp Ser Tyr Cys
 500 505 510
 Gly Val Gly Thr Ser Ile
 515

<210> 16

<211> 820

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 16

Met Leu Ala Ala Leu Ala Thr Ser Gln Leu Val Ala Thr Arg Ala Gly
 1 5 10 15
 Leu Gly Val Pro Asp Ala Ser Thr Phe Arg Arg Gly Ala Ala Gln Gly
 20 25 30
 Leu Arg Gly Ala Arg Ala Ser Ala Ala Asp Thr Leu Ser Met Arg
 35 40 45
 Thr Ser Ala Arg Ala Ala Pro Arg His Gln His Gln Gln Ala Arg Arg
 50 55 60
 Gly Ala Arg Phe Pro Ser Leu Val Val Cys Ala Ser Ala Gly Ala Met
 65 70 75 80
 Ala Lys Tyr Leu Glu Leu Glu Gly Gly Val Ile Met Gln Ala Phe
 85 90 95
 Tyr Trp Asp Val Pro Ser Gly Gly Ile Trp Trp Asp Thr Ile Arg Gln
 100 105 110
 Lys Ile Pro Glu Trp Tyr Asp Ala Gly Ile Ser Ala Ile Trp Ile Pro
 115 120 125
 Pro Ala Ser Lys Gly Met Ser Gly Gly Tyr Ser Met Gly Tyr Asp Pro
 130 135 140
 Tyr Asp Tyr Phe Asp Leu Gly Glu Tyr Tyr Gln Lys Gly Thr Val Glu
 145 150 155 160
 Thr Arg Phe Gly Ser Lys Gln Glu Leu Ile Asn Met Ile Asn Thr Ala
 165 170 175
 His Ala Tyr Gly Ile Lys Val Ile Ala Asp Ile Val Ile Asn His Arg
 180 185 190
 Ala Gly Gly Asp Leu Glu Trp Asn Pro Phe Val Gly Asp Tyr Thr Trp
 195 200 205
 Thr Asp Phe Ser Lys Val Ala Ser Gly Lys Tyr Thr Ala Asn Tyr Leu
 210 215 220
 Asp Phe His Pro Asn Glu His Ala Gly Asp Ser Gly Thr Phe Gly
 225 230 235 240
 Gly Tyr Pro Asp Ile Cys His Asp Lys Ser Trp Asp Gln Tyr Trp Leu
 245 250 255
 Trp Ala Ser Gln Glu Ser Tyr Ala Ala Tyr Leu Arg Ser Ile Gly Ile
 260 265 270
 Asp Ala Trp Arg Phe Asp Tyr Val Lys Gly Tyr Gly Ala Trp Val Val
 275 280 285

60110USPCT1 Corrected SEQ LIST 2-2007.txt

Lys Asp Trp Leu Asn Trp Trp Gly Gly Trp Ala Val Gly Glu Tyr Trp
 290 295 300
 Asp Thr Asn Val Asp Ala Leu Leu Asn Trp Ala Tyr Ser Ser Gly Ala
 305 310 315 320
 Lys Val Phe Asp Phe Pro Leu Tyr Tyr Lys Met Asp Ala Ala Phe Asp
 325 330 335
 Asn Lys Asn Ile Pro Ala Leu Val Glu Ala Leu Lys Asn Gly Gly Thr
 340 345 350
 Val Val Ser Arg Asp Pro Phe Lys Ala Val Thr Phe Val Ala Asn His
 355 360 365
 Asp Thr Asp Ile Ile Trp Asn Lys Tyr Pro Ala Tyr Ala Phe Ile Leu
 370 375 380
 Thr Tyr Glu Gly Gln Pro Thr Ile Phe Tyr Arg Asp Tyr Glu Glu Trp
 385 390 395 400
 Leu Asn Lys Asp Lys Leu Lys Asn Leu Ile Trp Ile His Asp Asn Leu
 405 410 415
 Ala Gly Gly Ser Thr Ser Ile Val Tyr Tyr Asp Ser Asp Glu Met Ile
 420 425 430
 Phe Val Arg Asn Gly Tyr Gly Ser Lys Pro Gly Leu Ile Thr Tyr Ile
 435 440 445
 Asn Leu Gly Ser Ser Lys Val Gly Arg Trp Val Tyr Val Pro Lys Phe
 450 455 460
 Ala Gly Ala Cys Ile His Glu Tyr Thr Gly Asn Leu Gly Gly Trp Val
 465 470 475 480
 Asp Lys Tyr Val Tyr Ser Ser Gly Trp Val Tyr Leu Glu Ala Pro Ala
 485 490 495
 Tyr Asp Pro Ala Asn Gly Gln Tyr Gly Tyr Ser Val Trp Ser Tyr Cys
 500 505 510
 Gly Val Gly Thr Ser Ile Ala Gly Ile Leu Glu Ala Asp Arg Val Leu
 515 520 525
 Thr Val Ser Pro Tyr Tyr Ala Glu Glu Leu Ile Ser Gly Ile Ala Arg
 530 535 540
 Gly Cys Glu Leu Asp Asn Ile Met Arg Leu Thr Gly Ile Thr Gly Ile
 545 550 555 560
 Val Asn Gly Met Asp Val Ser Glu Trp Asp Pro Ser Arg Asp Lys Tyr
 565 570 575
 Ile Ala Val Lys Tyr Asp Val Ser Thr Ala Val Glu Ala Lys Ala Leu
 580 585 590
 Asn Lys Glu Ala Leu Gln Ala Glu Val Gly Leu Pro Val Asp Arg Asn
 595 600 605
 Ile Pro Leu Val Ala Phe Ile Gly Arg Leu Glu Glu Gln Lys Gly Pro
 610 615 620
 Asp Val Met Ala Ala Ala Ile Pro Gln Leu Met Glu Met Val Glu Asp
 625 630 635 640
 Val Gln Ile Val Leu Glu Gly Thr Gly Lys Lys Phe Glu Arg Met
 645 650 655
 Leu Met Ser Ala Glu Glu Lys Phe Pro Gly Lys Val Arg Ala Val Val
 660 665 670
 Lys Phe Asn Ala Ala Leu Ala His His Ile Met Ala Gly Ala Asp Val
 675 680 685
 Leu Ala Val Thr Ser Arg Phe Glu Pro Cys Gly Leu Ile Gln Leu Gln
 690 695 700
 Gly Met Arg Tyr Gly Thr Pro Cys Ala Cys Ala Ser Thr Gly Gly Leu
 705 710 715 720
 Val Asp Thr Ile Ile Glu Gly Lys Thr Gly Phe His Met Gly Arg Leu
 725 730 735
 Ser Val Asp Cys Asn Val Val Glu Pro Ala Asp Val Lys Lys Val Ala
 740 745 750
 Thr Thr Leu Gln Arg Ala Ile Lys Val Val Gly Thr Pro Ala Tyr Glu
 755 760 765
 Glu Met Val Arg Asn Cys Met Ile Gln Asp Leu Ser Trp Lys Gly Pro
 770 775 780
 Ala Lys Asn Trp Glu Asn Val Leu Leu Ser Leu Gly Val Ala Gly Gly

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785
Glu Pro Gly Val Glu Gly Glu Glu Ile Ala Pro Leu Ala Lys Glu Asn
805 810 815 820

<210> 17
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 17
Met Arg Val Leu Leu Val Ala Leu Ala Leu Leu Ala Leu Ala Ala Ser
1 5 10 15
Ala Thr Ser

<210> 18
<211> 444
<212> PRT
<213> Thermotoga maritima

<400> 18
Met Ala Glu Phe Phe Pro Glu Ile Pro Lys Ile Gln Phe Glu Gly Lys
1 5 10 15
Glu Ser Thr Asn Pro Leu Ala Phe Arg Phe Tyr Asp Pro Asn Glu Val
20 25 30
Ile Asp Gly Lys Pro Leu Lys Asp His Leu Lys Phe Ser Val Ala Phe
35 40 45
Trp His Thr Phe Val Asn Glu Gly Arg Asp Pro Phe Gly Asp Pro Thr
50 55 60
Ala Glu Arg Pro Trp Asn Arg Phe Ser Asp Pro Met Asp Lys Ala Phe
65 70 75 80
Ala Arg Val Asp Ala Leu Phe Glu Phe Cys Glu Lys Leu Asn Ile Glu
85 90 95
Tyr Phe Cys Phe His Asp Arg Asp Ile Ala Pro Glu Gly Lys Thr Leu
100 105 110
Arg Glu Thr Asn Lys Ile Leu Asp Lys Val Val Glu Arg Ile Lys Glu
115 120 125
Arg Met Lys Asp Ser Asn Val Lys Leu Leu Trp Gly Thr Ala Asn Leu
130 135 140
Phe Ser His Pro Arg Tyr Met His Gly Ala Ala Thr Thr Cys Ser Ala
145 150 155 160
Asp Val Phe Ala Tyr Ala Ala Ala Gln Val Lys Lys Ala Leu Glu Ile
165 170 175
Thr Lys Glu Leu Gly Gly Glu Gly Tyr Val Phe Trp Gly Gly Arg Glu
180 185 190
Gly Tyr Glu Thr Leu Leu Asn Thr Asp Leu Gly Leu Glu Leu Glu Asn
195 200 205
Leu Ala Arg Phe Leu Arg Met Ala Val Glu Tyr Ala Lys Lys Ile Gly
210 215 220
Phe Thr Gly Gln Phe Leu Ile Glu Pro Lys Pro Lys Glu Pro Thr Lys
225 230 235 240
His Gln Tyr Asp Phe Asp Val Ala Thr Ala Tyr Ala Phe Leu Lys Asn
245 250 255
His Gly Leu Asp Glu Tyr Phe Lys Phe Asn Ile Glu Ala Asn His Ala
260 265 270
Thr Leu Ala Gly His Thr Phe Gln His Glu Leu Arg Met Ala Arg Ile
275 280 285

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Leu Gly Lys Leu Gly Ser Ile Asp Ala Asn Gln Gly Asp Leu Leu Leu
 290 295 300
 Gly Trp Asp Thr Asp Gln Phe Pro Thr Asn Ile Tyr Asp Thr Thr Leu
 305 310 315 320
 Ala Met Tyr Glu Val Ile Lys Ala Gly Gly Phe Thr Lys Gly Gly Leu
 325 330 335
 Asn Phe Asp Ala Lys Val Arg Arg Ala Ser Tyr Lys Val Glu Asp Leu
 340 345 350
 Phe Ile Gly His Ile Ala Gly Met Asp Thr Phe Ala Leu Gly Phe Lys
 355 360 365
 Ile Ala Tyr Lys Leu Ala Lys Asp Gly Val Phe Asp Lys Phe Ile Glu
 370 375 380
 Glu Lys Tyr Arg Ser Phe Lys Glu Gly Ile Gly Lys Glu Ile Val Glu
 385 390 395 400
 Gly Lys Thr Asp Phe Glu Lys Leu Glu Tyr Ile Ile Asp Lys Glu
 405 410 415
 Asp Ile Glu Leu Pro Ser Gly Lys Gln Glu Tyr Leu Glu Ser Leu Leu
 420 425 430
 Asn Ser Tyr Ile Val Lys Thr Ile Ala Glu Leu Arg
 435 440

<210> 19

<211> 1335

<212> DNA

<213> *Thermotoga maritima*

<400> 19

atggccgagt tcttcccga gatcccgaag atccagttcg agggcaagga gtccaccaac 60
 ccgctcgcct tccgcttcta cgacccgaac gaggtgatcg acggcaagcc gctcaaggac 120
 cacctcaagt tctccgtggc cttctggcac acctcgtga acgagggccg cgacccgttc 180
 ggcgaccga ccgccgagcg cccgtggaac cgtttctccg acccgatgga caaggccttc 240
 gccgcgtgg acgcccctct cgagttctgc gagaagctca acatcgagta cttctgcttc 300
 caccgaccgc acatcgcccc ggagggcaag accctccgcg agaccaacaa gatcctcgac 360
 aaggtggtgg agcgcatcaa ggagcgcgat aaggactcca acgtgaagct cctctggggc 420
 accgccaacc tcttctccca cccgcgctac atgcacggcg ccgccaccac ctgctccgcc 480
 gacgtgttcg cctacgccgc cgcccagggt aagaaggccc tggagatcac caaggagctg 540
 ggcggcgagg gctacgtgtt ctggggcggc cgcgagggt acgagaccct cctcaacacc 600
 gacctcgcc tggagctgga gaacctcgcc cgcttctcc gcatggccgt ggagtacgcc 660
 aagaagatcg gcttcaccgg ccagttcttc atcgagccga agccgaagga gccgaccaag 720
 caccagtacg acttcgacgt ggccaccgcc tacgccttcc tcaagaacca cggcctcgac 780
 gagtacttca agttcaacat cgaggccaac cagccacccc tcgcccggcca caccttccag 840
 caccgagctg gcatggcccc catcctcggc aagctcggct ccacgcacgc caaccagggc 900
 gacctcttc tcggctggga caccgaccg ttcccacca acatctacga caccaccctc 960
 gccatgtacg aggtgatcaa ggccgcgccg ttcaccaagg gcggcctcaa cttcgacgcc 1020
 aaggtgcgcc gcgcctccta caaggtggag gacctcttca tcggccacat cgccggcatg 1080
 gacaccttcg cctcggcgt caagatcgcc tacaagctcg ccaaggacgg cgtgttcgac 1140
 aagttcatcg aggagaagta ccgctccttc aaggagggca tcggcaagga gatcgtggag 1200
 ggcaagaccg acttcgagaa gctggaggag tacatcatcg acaaggagga catcgagctg 1260
 ccgtccggca agcaggagta cctggagtc ctcctcaact cctacatcgt gaagaccatc 1320
 gccgagctgc gctga 1335

<210> 20

<211> 444

<212> PRT

<213> *Thermotoga neapolitana*

<400> 20

Met Ala Glu Phe Phe Pro Glu Ile Pro Lys Val Gln Phe Glu Gly Lys
 1 5 10 15
 Glu Ser Thr Asn Pro Leu Ala Phe Lys Phe Tyr Asp Pro Glu Glu Ile
 20 25 30
 Ile Asp Gly Lys Pro Leu Lys Asp His Leu Lys Phe Ser Val Ala Phe

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35 40 45
 Trp His Thr Phe Val Asn Glu Gly Arg Asp Pro Phe Gly Asp Pro Thr
 50 55 60
 Ala Asp Arg Pro Trp Asn Arg Tyr Thr Asp Pro Met Asp Lys Ala Phe
 65 70 75 80
 Ala Arg Val Asp Ala Leu Phe Glu Phe Cys Glu Lys Leu Asn Ile Glu
 85 90 95
 Tyr Phe Cys Phe His Asp Arg Asp Ile Ala Pro Glu Gly Lys Thr Leu
 100 105 110
 Arg Glu Thr Asn Lys Ile Leu Asp Lys Val Val Glu Arg Ile Lys Glu
 115 120 125
 Arg Met Lys Asp Ser Asn Val Lys Leu Leu Trp Gly Thr Ala Asn Leu
 130 135 140
 Phe Ser His Pro Arg Tyr Met His Gly Ala Ala Thr Thr Cys Ser Ala
 145 150 155 160
 Asp Val Phe Ala Tyr Ala Ala Ala Gln Val Lys Lys Ala Leu Glu Ile
 165 170 175
 Thr Lys Glu Leu Gly Gly Glu Gly Tyr Val Phe Trp Gly Gly Arg Glu
 180 185 190
 Gly Tyr Glu Thr Leu Leu Asn Thr Asp Leu Gly Phe Glu Leu Glu Asn
 195 200 205
 Leu Ala Arg Phe Leu Arg Met Ala Val Asp Tyr Ala Lys Arg Ile Gly
 210 215 220
 Phe Thr Gly Gln Phe Leu Ile Glu Pro Lys Pro Lys Glu Pro Thr Lys
 225 230 235 240
 His Gln Tyr Asp Phe Asp Val Ala Thr Ala Tyr Ala Phe Leu Lys Ser
 245 250 255
 His Gly Leu Asp Glu Tyr Phe Lys Phe Asn Ile Glu Ala Asn His Ala
 260 265 270
 Thr Leu Ala Gly His Thr Phe Gln His Glu Leu Arg Met Ala Arg Ile
 275 280 285
 Leu Gly Lys Leu Gly Ser Ile Asp Ala Asn Gln Gly Asp Leu Leu Leu
 290 295 300
 Gly Trp Asp Thr Asp Gln Phe Pro Thr Asn Val Tyr Asp Thr Thr Leu
 305 310 315 320
 Ala Met Tyr Glu Val Ile Lys Ala Gly Gly Phe Thr Lys Gly Gly Leu
 325 330 335
 Asn Phe Asp Ala Lys Val Arg Arg Ala Ser Tyr Lys Val Glu Asp Leu
 340 345 350
 Phe Ile Gly His Ile Ala Gly Met Asp Thr Phe Ala Leu Gly Phe Lys
 355 360 365
 Val Ala Tyr Lys Leu Val Lys Asp Gly Val Leu Asp Lys Phe Ile Glu
 370 375 380
 Glu Lys Tyr Arg Ser Phe Arg Glu Gly Ile Gly Arg Asp Ile Val Glu
 385 390 395 400
 Gly Lys Val Asp Phe Glu Lys Leu Glu Glu Tyr Ile Ile Asp Lys Glu
 405 410 415
 Thr Ile Glu Leu Pro Ser Gly Lys Gln Glu Tyr Leu Glu Ser Leu Ile
 420 425 430
 Asn Ser Tyr Ile Val Lys Thr Ile Leu Glu Leu Arg
 435 440

<210> 21

<211> 1335

<212> DNA

<213> Thermotoga neapolitana

<400> 21

atggccgagt tcttcccga gatcccgaag gtgcagttcg agggcaagga gtccaccaac 60
 ccgctcgctt tcaagttcta cgaccggag gagatcatcg acggcaagcc gctcaaggac 120
 cacctcaagt tctccgtggc cttctggcac accttcgtga acgagggccg cgaccggttc 180
 ggcgaccga ccgcccaccg cccgtggaac cgctacaccg acccgatgga caaggccttc 240

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gcccgcgtgg acgccctctt cgagttctgc gagaagctca acatcgagta cttctgcttc 300
cacgaccgcg acatcgcccc ggagggcaag accctccgcg agaccaacaa gatcctcgac 360
aagggtggtg agcgcatcaa ggagcgcatg aaggactcca acgtgaagct cctctggggc 420
accgccaacc tcttctccca cccgcgctac atgcacggcg ccgccaccac ctgctccgcc 480
gacgtgttcg cctacgccgc cgcccagggtg aagaaggccc tggagatcac caaggagctg 540
ggcggcgagg gctacgtgtt ctggggcggc cgcgagggtt acgagaccct cctcaacacc 600
gacctcggct tcgagctgga gaacctcgcc cgcttcctcc gcatggccgt ggactacgcc 660
aagcgcatcg gcttcaccgg ccagttcctc atcgagccga agccgaagga gccgaccaag 720
caccagtacg acttcgacgt ggccaccgcc tacgccttc tcaagtcca cggcctcgac 780
gagtacttca agttcaaac cgaggccaac cacgccacc tcgccggcca cacttccag 840
cacgagctgc gcatggcccc catcctcggc aagctcggct ccatcgacgc caaccagggc 900
gacctcctcc tcggctggga caccgaccag ttcccgacca acgtgtacga caccaccctc 960
gccatgtacg aggtgatcaa ggccggcggc ttcaccaagg gcggcctcaa cttcgacgcc 1020
aagggtgcgc gcgcctccta caagggtggag gacctcttca tcggccacat cgccggcatg 1080
gacaccttcg ccttcggctt caaggtggcc tacaagctcg tgaaggacgg cgtgctcgac 1140
aagttcatcg aggagaagta ccgctccttc cgcgagggca tcggccgcga catcgtggag 1200
ggcaagggtg acttcgagaa gctggaggag tacatcatcg acaaggagac catcgagctg 1260
ccgtccggca agcaggagta cctggagtcc ctcatcaact cctacatcgt gaagaccatc 1320
ctggagctgc gctga                                     1335

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<210> 22

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 22

agcgaattca tggcggctct ggccacgt

28

<210> 23

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 23

agctaagctt cagggcgcgg ccacgttct

29

<210> 24

<211> 825

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 24

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Met Arg Val Leu Leu Val Ala Leu Ala Leu Leu Ala Leu Ala Ala Ser
 1           5           10          15
Ala Thr Ser Ala Gly His Trp Tyr Lys His Gln Arg Ala Tyr Gln Phe
 20          25          30
Thr Gly Glu Asp Asp Phe Gly Lys Val Ala Val Val Lys Leu Pro Met
 35          40          45
Asp Leu Thr Lys Val Gly Ile Ile Val Arg Leu Asn Glu Trp Gln Ala
 50          55          60
Lys Asp Val Ala Lys Asp Arg Phe Ile Glu Ile Lys Asp Gly Lys Ala
 65          70          75          80
Glu Val Trp Ile Leu Gln Gly Val Glu Glu Ile Phe Tyr Glu Lys Pro
 85          90          95

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60110USPCT1 Corrected SEQ LIST 2-2007.txt

Asp	Thr	Ser	Pro	Arg	Ile	Phe	Phe	Ala	Gln	Ala	Arg	Ser	Asn	Lys	Val
			100					105					110		
Ile	Glu	Ala	Phe	Leu	Thr	Asn	Pro	Val	Asp	Thr	Lys	Lys	Lys	Glu	Leu
		115					120					125			
Phe	Lys	Val	Thr	Val	Asp	Gly	Lys	Glu	Ile	Pro	Val	Ser	Arg	Val	Glu
	130					135					140				
Lys	Ala	Asp	Pro	Thr	Asp	Ile	Asp	Val	Thr	Asn	Tyr	Val	Arg	Ile	Val
145					150					155				160	
Leu	Ser	Glu	Ser	Leu	Lys	Glu	Glu	Asp	Leu	Arg	Lys	Asp	Val	Glu	Leu
				165					170					175	
Ile	Ile	Glu	Gly	Tyr	Lys	Pro	Ala	Arg	Val	Ile	Met	Met	Glu	Ile	Leu
			180					185					190		
Asp	Asp	Tyr	Tyr	Tyr	Asp	Gly	Glu	Leu	Gly	Ala	Val	Tyr	Ser	Pro	Glu
		195					200					205			
Lys	Thr	Ile	Phe	Arg	Val	Trp	Ser	Pro	Val	Ser	Lys	Trp	Val	Lys	Val
	210					215					220				
Leu	Leu	Phe	Lys	Asn	Gly	Glu	Asp	Thr	Glu	Pro	Tyr	Gln	Val	Val	Asn
225					230					235					240
Met	Glu	Tyr	Lys	Gly	Asn	Gly	Val	Trp	Glu	Ala	Val	Val	Glu	Gly	Asp
				245					250					255	
Leu	Asp	Gly	Val	Phe	Tyr	Leu	Tyr	Gln	Leu	Glu	Asn	Tyr	Gly	Lys	Ile
			260					265					270		
Arg	Thr	Thr	Val	Asp	Pro	Tyr	Ser	Lys	Ala	Val	Tyr	Ala	Asn	Asn	Gln
		275					280					285			
Glu	Ser	Ala	Val	Val	Asn	Leu	Ala	Arg	Thr	Asn	Pro	Glu	Gly	Trp	Glu
					295						300				
Asn	Asp	Arg	Gly	Pro	Lys	Ile	Glu	Gly	Tyr	Glu	Asp	Ala	Ile	Ile	Tyr
305					310					315					320
Glu	Ile	His	Ile	Ala	Asp	Ile	Thr	Gly	Leu	Glu	Asn	Ser	Gly	Val	Lys
				325					330					335	
Asn	Lys	Gly	Leu	Tyr	Leu	Gly	Leu	Thr	Glu	Glu	Asn	Thr	Lys	Ala	Pro
				340				345					350		
Gly	Gly	Val	Thr	Thr	Gly	Leu	Ser	His	Leu	Val	Glu	Leu	Gly	Val	Thr
		355					360					365			
His	Val	His	Ile	Leu	Pro	Phe	Phe	Asp	Phe	Tyr	Thr	Gly	Asp	Glu	Leu
		370				375					380				
Asp	Lys	Asp	Phe	Glu	Lys	Tyr	Tyr	Asn	Trp	Gly	Tyr	Asp	Pro	Tyr	Leu
385					390					395					400
Phe	Met	Val	Pro	Glu	Gly	Arg	Tyr	Ser	Thr	Asp	Pro	Lys	Asn	Pro	His
				405					410					415	
Thr	Arg	Ile	Arg	Glu	Val	Lys	Glu	Met	Val	Lys	Ala	Leu	His	Lys	His
			420					425					430		
Gly	Ile	Gly	Val	Ile	Met	Asp	Met	Val	Phe	Pro	His	Thr	Tyr	Gly	Ile
			435				440					445			
Gly	Glu	Leu	Ser	Ala	Phe	Asp	Gln	Thr	Val	Pro	Tyr	Tyr	Phe	Tyr	Arg
					455					460					
Ile	Asp	Lys	Thr	Gly	Ala	Tyr	Leu	Asn	Glu	Ser	Gly	Cys	Gly	Asn	Val
465					470					475					480
Ile	Ala	Ser	Glu	Arg	Pro	Met	Met	Arg	Lys	Phe	Ile	Val	Asp	Thr	Val
				485					490					495	
Thr	Tyr	Trp	Val	Lys	Glu	Tyr	His	Ile	Asp	Gly	Phe	Arg	Phe	Asp	Gln
			500					505					510		
Met	Gly	Leu	Ile	Asp	Lys	Lys	Thr	Met	Leu	Glu	Val	Glu	Arg	Ala	Leu
			515				520					525			
His	Lys	Ile	Asp	Pro	Thr	Ile	Ile	Leu	Tyr	Gly	Glu	Pro	Trp	Gly	Gly
	530					535					540				
Trp	Gly	Ala	Pro	Ile	Arg	Phe	Gly	Lys	Ser	Asp	Val	Ala	Gly	Thr	His
545					550					555					560
Val	Ala	Ala	Phe	Asn	Asp	Glu	Phe	Arg	Asp	Ala	Ile	Arg	Gly	Ser	Val
				565					570					575	
Phe	Asn	Pro	Ser	Val	Lys	Gly	Phe	Val	Met	Gly	Gly	Tyr	Gly	Lys	Glu
			580					585					590		
Thr	Lys	Ile	Lys	Arg	Gly	Val	Val	Gly	Ser	Ile	Asn	Tyr	Asp	Gly	Lys

60110USPCT1 Corrected SEQ LIST 2-2007.txt

Leu	Ile	Lys	Ser	Phe	Ala	Leu	Asp	Pro	Glu	Glu	Thr	Ile	Asn	Tyr	Ala
610	610	610	610	610	610	615	615	615	615	615	620	620	620	620	620
Ala	Cys	His	Asp	Asn	His	Thr	Leu	Trp	Asp	Lys	Asn	Tyr	Leu	Ala	Ala
625	625	625	625	625	630	630	630	630	630	635	635	635	635	640	640
Lys	Ala	Asp	Lys	Lys	Lys	Glu	Trp	Thr	Glu	Glu	Glu	Leu	Lys	Asn	Ala
				645	645	645	645	645	650	650	650	650	650	655	655
Gln	Lys	Leu	Ala	Gly	Ala	Ile	Leu	Leu	Thr	Ser	Gln	Gly	Val	Pro	Phe
			660	660	660	660	665	665	665	665	665	665	670	670	670
Leu	His	Gly	Gly	Gln	Asp	Phe	Cys	Arg	Thr	Thr	Asn	Phe	Asn	Asp	Asn
		675	675	675	675	675	680	680	680	680	685	685	685	685	685
Ser	Tyr	Asn	Ala	Pro	Ile	Ser	Ile	Asn	Gly	Phe	Asp	Tyr	Glu	Arg	Lys
	690	690	690	690	690	695	695	695	695	695	700	700	700	700	700
Leu	Gln	Phe	Ile	Asp	Val	Phe	Asn	Tyr	His	Lys	Gly	Leu	Ile	Lys	Leu
705	705	705	705	705	710	710	710	710	710	715	715	715	715	720	720
Arg	Lys	Glu	His	Pro	Ala	Phe	Arg	Leu	Lys	Asn	Ala	Glu	Glu	Ile	Lys
				725	725	725	725	725	730	730	730	730	730	735	735
Lys	His	Leu	Glu	Phe	Leu	Pro	Gly	Gly	Arg	Arg	Ile	Val	Ala	Phe	Met
			740	740	740	740	745	745	745	745	745	745	750	750	750
Leu	Lys	Asp	His	Ala	Gly	Gly	Asp	Pro	Trp	Lys	Asp	Ile	Val	Val	Ile
		755	755	755	755	755	760	760	760	760	765	765	765	765	765
Tyr	Asn	Gly	Asn	Leu	Glu	Lys	Thr	Thr	Tyr	Lys	Leu	Pro	Glu	Gly	Lys
	770	770	770	770	770	775	775	775	775	775	780	780	780	780	780
Trp	Asn	Val	Val	Val	Asn	Ser	Gln	Lys	Ala	Gly	Thr	Glu	Val	Ile	Glu
785	785	785	785	785	790	790	790	790	790	795	795	795	795	800	800
Thr	Val	Glu	Gly	Thr	Ile	Glu	Leu	Asp	Pro	Leu	Ser	Ala	Tyr	Val	Leu
				805	805	805	805	805	810	810	810	810	810	815	815
Tyr	Arg	Glu	Ser	Glu	Lys	Asp	Glu	Leu							
			820	820	820	820	825	825							

<210> 25

<211> 2478

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 25

atgaggggtgt	tgctcgttgc	cctcgccttc	ctggctctcg	ctgcgagcgc	caccagcgct	60
ggccactgggt	acaagcacca	gcgcgcctac	cagttcaccg	gcgaggacga	cttcgggaag	120
gtggccgtgg	tgaagctccc	gatggacctc	accaaggtgg	gcatcatcgt	gcgcctcaac	180
gagtgccagg	cgaaggacgt	ggccaaggac	cgcttcacgc	agatcaagga	cggcaaggcc	240
gaggtgtgga	tactccaggg	cgtggaggag	atcttctacg	agaagccgga	cacctccccg	300
cgcattctct	tcgcccaggc	ccgctccaac	aaggtgatcg	aggccttcct	caccaaccgc	360
gtggacacca	agaagaagga	gctgttcaag	gtgaccgtcg	acggcaagga	gatcccgggtg	420
tcccgcgtgg	agaaggccga	cccgaaccac	atcgacgtga	ccaactacgt	gcgcatcgtg	480
ctctccgagt	ccctcaagga	ggaggacctc	cgcaaggacg	tggagctgat	catcgagggc	540
tacaagccgg	cccgcgtgat	catgatggag	atcctcgacg	actactacta	cgacggcgag	600
ctgggggccc	tgtactcccc	ggagaagacc	atcttccgcg	tgtgggtccc	ggtgtccaag	660
tgggtgaagg	tgctcctctt	caagaacggc	gaggacaccg	agccgtacca	ggtggtgaac	720
atggagtaca	agggcaacgg	cgtgtgggag	gccgtgggtg	agggcgacct	cgacggcggtg	780
ttctacctct	accagctgga	gaactacggc	aagatccgca	ccaccgtgga	cccgtactcc	840
aaggccgtgt	acgccaacaa	ccaggagtct	gcagtgggtg	acctcgcccc	caccaaccgc	900
gagggctggg	agaacgacgg	cggcccgaag	atcgagggct	acgaggacgc	catcatctac	960
gagatccaca	tcgccgacat	caccggcctg	gagaactccg	gcgtgaagaa	caagggcctc	1020
tacctcggcc	tcaccgagga	gaacaccaag	gccccgggcg	gcgtgaccac	cggcctctcc	1080
cacctcgtgg	agctgggcgt	gacccacgtg	cacatcctcc	cgttcttcga	cttctacacc	1140
ggcgacgagc	tggacaagga	cttcgagaag	tactacaact	ggggctacga	cccgtacctc	1200
ttcatggtgc	cggagggcct	ctactccacc	gaaccgaaga	acccgcacac	ccgaattcgc	1260
gaggtgaagg	agatggtgaa	ggccctccac	aagcacggca	tcggcggtgat	catggacatg	1320
gtgttcccgc	acacctacgg	catcggcgag	ctgtccgcct	tcgaccagac	cgtgccgtac	1380

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tacttctacc gcatcgacaa gaccggcgcc tacctcaacg agtccggctg cggcaacgtg 1440
atcgctcccg agcgcccgat gatgcgcaag ttcatcgtgg acaccgtgac ctactgggtg 1500
aaggagtagc acatcgacgg cttccgcttc gaccagatgg gcctcatcga caagaagacc 1560
atgctggagg tggagcgcg cctccacaag atcgacccga ccatcatcct ctacggcgag 1620
ccgtggggcg gctggggggc cccgatccgc ttcggcaagt ccgacgtggc cggcaccac 1680
gtggccgctt tcaacgacga gttccgcgac gccatccgag gctccgtgtt caaccgtcc 1740
gtgaagggtc tcgtgatggg cggctacggc aaggagacca agatcaagcg cggcgtggtg 1800
ggctccatca actacgacgg caagctcatc aagtccttcg ccctcgaccc ggaggagacc 1860
atcaactacg ccgcttgcca cgacaaccac accctctggg acaagaacta cctcgccgcc 1920
aaggccgaca agaagaagga gtggaccgag gaggagctga agaacgcca gaagctcgcc 1980
ggcgccatcc tcctcactag tcagggcgtg ccgttcctcc acggcgcca ggacttctgc 2040
cgaccacca acttcaacga caactcctac aacgccccga tctccatcaa cggcttcgac 2100
tacgagcgca agctccagtt catcgacgtg ttcaactacc acaagggcct catcaagctc 2160
cgcaaggagc acccgccctt ccgctcaag aacgcccagg agatcaagaa gcacctggag 2220
ttcctcccgg gcgggcgccg catcgtggcc ttcattgctca aggaccacgc cggcgcgac 2280
ccgtggaagg acatcgtggt gatctacaac ggcaacctgg agaagaccac ctacaagctc 2340
ccggagggca agtggaacgt ggtggtgaac tcccagaagg ccggcaccga ggtgatcgag 2400
accgtggagg gcaccatcga gctggaccgg ctctccgcct acgtgctcta ccgcgagtcc 2460
gagaaggacg agctgtga 2478

```

<210> 26

<211> 718

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 26

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Met Arg Val Leu Leu Val Ala Leu Ala Leu Leu Ala Leu Ala Ala Ser
1      5      10      15
Ala Thr Ser Met Glu Thr Ile Lys Ile Tyr Glu Asn Lys Gly Val Tyr
20      25      30
Lys Val Val Ile Gly Glu Pro Phe Pro Pro Ile Glu Phe Pro Leu Glu
35      40      45
Gln Lys Ile Ser Ser Asn Lys Ser Leu Ser Glu Leu Gly Leu Thr Ile
50      55      60
Val Gln Gln Gly Asn Lys Val Ile Val Glu Lys Ser Leu Asp Leu Lys
65      70      75      80
Glu His Ile Ile Gly Leu Gly Glu Lys Ala Phe Glu Leu Asp Arg Lys
85      90      95
Arg Lys Arg Tyr Val Met Tyr Asn Val Asp Ala Gly Ala Tyr Lys Lys
100     105     110
Tyr Gln Asp Pro Leu Tyr Val Ser Ile Pro Leu Phe Ile Ser Val Lys
115     120     125
Asp Gly Val Ala Thr Gly Tyr Phe Phe Asn Ser Ala Ser Lys Val Ile
130     135     140
Phe Asp Val Gly Leu Glu Glu Tyr Asp Lys Val Ile Val Thr Ile Pro
145     150     155     160
Glu Asp Ser Val Glu Phe Tyr Val Ile Glu Gly Pro Arg Ile Glu Asp
165     170     175
Val Leu Glu Lys Tyr Thr Glu Leu Thr Gly Lys Pro Phe Leu Pro Pro
180     185     190
Met Trp Ala Phe Gly Tyr Met Ile Ser Arg Tyr Ser Tyr Tyr Pro Gln
195     200     205
Asp Lys Val Val Glu Leu Val Asp Ile Met Gln Lys Glu Gly Phe Arg
210     215     220
Val Ala Gly Val Phe Leu Asp Ile His Tyr Met Asp Ser Tyr Lys Leu
225     230     235     240
Phe Thr Trp His Pro Tyr Arg Phe Pro Glu Pro Lys Lys Leu Ile Asp
245     250     255
Glu Leu His Lys Arg Asn Val Lys Leu Ile Thr Ile Val Asp His Gly
260     265     270

```


60110USPCT1 Corrected SEQ LIST 2-2007.txt

```

Ile Arg Val Asp Gln Asn Tyr Ser Pro Phe Leu Ser Gly Met Gly Lys
275 280 285
Phe Cys Glu Ile Glu Ser Gly Glu Leu Phe Val Gly Lys Met Trp Pro
290 295 300
Gly Thr Thr Val Tyr Pro Asp Phe Phe Arg Glu Asp Thr Arg Glu Trp
305 310 315 320
Trp Ala Gly Leu Ile Ser Glu Trp Leu Ser Gln Gly Val Asp Gly Ile
325 330 335
Trp Leu Asp Met Asn Glu Pro Thr Asp Phe Ser Arg Ala Ile Glu Ile
340 345 350
Arg Asp Val Leu Ser Ser Leu Pro Val Gln Phe Arg Asp Asp Arg Leu
355 360 365
Val Thr Thr Phe Pro Asp Asn Val Val His Tyr Leu Arg Gly Lys Arg
370 375 380
Val Lys His Glu Lys Val Arg Asn Ala Tyr Pro Leu Tyr Glu Ala Met
385 390 395 400
Ala Thr Phe Lys Gly Phe Arg Thr Ser His Arg Asn Glu Ile Phe Ile
405 410 415
Leu Ser Arg Ala Gly Tyr Ala Gly Ile Gln Arg Tyr Ala Phe Ile Trp
420 425 430
Thr Gly Asp Asn Thr Pro Ser Trp Asp Asp Leu Lys Leu Gln Leu Gln
435 440 445
Leu Val Leu Gly Leu Ser Ile Ser Gly Val Pro Phe Val Gly Cys Asp
450 455 460
Ile Gly Gly Phe Gln Gly Arg Asn Phe Ala Glu Ile Asp Asn Ser Met
465 470 475 480
Asp Leu Leu Val Lys Tyr Tyr Ala Leu Ala Leu Phe Phe Pro Phe Tyr
485 490 495
Arg Ser His Lys Ala Thr Asp Gly Ile Asp Thr Glu Pro Val Phe Leu
500 505 510
Pro Asp Tyr Tyr Lys Glu Lys Val Lys Glu Ile Val Glu Leu Arg Tyr
515 520 525
Lys Phe Leu Pro Tyr Ile Tyr Ser Leu Ala Leu Glu Ala Ser Glu Lys
530 535 540
Gly His Pro Val Ile Arg Pro Leu Phe Tyr Glu Phe Gln Asp Asp Asp
545 550 555 560
Asp Met Tyr Arg Ile Glu Asp Glu Tyr Met Val Gly Lys Tyr Leu Leu
565 570 575
Tyr Ala Pro Ile Val Ser Lys Glu Glu Ser Arg Leu Val Thr Leu Pro
580 585 590
Arg Gly Lys Trp Tyr Asn Tyr Trp Asn Gly Glu Ile Ile Asn Gly Lys
595 600 605
Ser Val Val Lys Ser Thr His Glu Leu Pro Ile Tyr Leu Arg Glu Gly
610 615 620
Ser Ile Ile Pro Leu Glu Gly Asp Glu Leu Ile Val Tyr Gly Glu Thr
625 630 635 640
Ser Phe Lys Arg Tyr Asp Asn Ala Glu Ile Thr Ser Ser Ser Asn Glu
645 650 655
Ile Lys Phe Ser Arg Glu Ile Tyr Val Ser Lys Leu Thr Ile Thr Ser
660 665 670
Glu Lys Pro Val Ser Lys Ile Ile Val Asp Asp Ser Lys Glu Ile Gln
675 680 685
Val Glu Lys Thr Met Gln Asn Thr Tyr Val Ala Lys Ile Asn Gln Lys
690 695 700
Ile Arg Gly Lys Ile Asn Leu Glu Ser Glu Lys Asp Glu Leu
705 710 715

```

<210> 27

<211> 712

<212> PRT

<213> Artificial Sequence

60110USPCT1 Corrected SEQ LIST 2-2007.txt

<220>

<223> synthetic

<400> 27

Met Arg Val Leu Leu Val Ala Leu Ala Leu Leu Ala Leu Ala Ala Ser
 1 5 10 15
 Ala Thr Ser Met Glu Thr Ile Lys Ile Tyr Glu Asn Lys Gly Val Tyr
 20 25 30
 Lys Val Val Ile Gly Glu Pro Phe Pro Pro Ile Glu Phe Pro Leu Glu
 35 40 45
 Gln Lys Ile Ser Ser Asn Lys Ser Leu Ser Glu Leu Gly Leu Thr Ile
 50 55 60
 Val Gln Gln Gly Asn Lys Val Ile Val Glu Lys Ser Leu Asp Leu Lys
 65 70 75 80
 Glu His Ile Ile Gly Leu Gly Glu Lys Ala Phe Glu Leu Asp Arg Lys
 85 90 95
 Arg Lys Arg Tyr Val Met Tyr Asn Val Asp Ala Gly Ala Tyr Lys Lys
 100 105 110
 Tyr Gln Asp Pro Leu Tyr Val Ser Ile Pro Leu Phe Ile Ser Val Lys
 115 120 125
 Asp Gly Val Ala Thr Gly Tyr Phe Phe Asn Ser Ala Ser Lys Val Ile
 130 135 140
 Phe Asp Val Gly Leu Glu Glu Tyr Asp Lys Val Ile Val Thr Ile Pro
 145 150 155 160
 Glu Asp Ser Val Glu Phe Tyr Val Ile Glu Gly Pro Arg Ile Glu Asp
 165 170 175
 Val Leu Glu Lys Tyr Thr Glu Leu Thr Gly Lys Pro Phe Leu Pro Pro
 180 185 190
 Met Trp Ala Phe Gly Tyr Met Ile Ser Arg Tyr Ser Tyr Tyr Pro Gln
 195 200 205
 Asp Lys Val Val Glu Leu Val Asp Ile Met Gln Lys Glu Gly Phe Arg
 210 215 220
 Val Ala Gly Val Phe Leu Asp Ile His Tyr Met Asp Ser Tyr Lys Leu
 225 230 235 240
 Phe Thr Trp His Pro Tyr Arg Phe Pro Glu Pro Lys Lys Leu Ile Asp
 245 250 255
 Glu Leu His Lys Arg Asn Val Lys Leu Ile Thr Ile Val Asp His Gly
 260 265 270
 Ile Arg Val Asp Gln Asn Tyr Ser Pro Phe Leu Ser Gly Met Gly Lys
 275 280 285
 Phe Cys Glu Ile Glu Ser Gly Glu Leu Phe Val Gly Lys Met Trp Pro
 290 295 300
 Gly Thr Thr Val Tyr Pro Asp Phe Phe Arg Glu Asp Thr Arg Glu Trp
 305 310 315 320
 Trp Ala Gly Leu Ile Ser Glu Trp Leu Ser Gln Gly Val Asp Gly Ile
 325 330 335
 Trp Leu Asp Met Asn Glu Pro Thr Asp Phe Ser Arg Ala Ile Glu Ile
 340 345 350
 Arg Asp Val Leu Ser Ser Leu Pro Val Gln Phe Arg Asp Arg Arg Leu
 355 360 365
 Val Thr Thr Phe Pro Asp Asn Val Val His Tyr Leu Arg Gly Lys Arg
 370 375 380
 Val Lys His Glu Lys Val Arg Asn Ala Tyr Pro Leu Tyr Glu Ala Met
 385 390 395 400
 Ala Thr Phe Lys Gly Phe Arg Thr Ser His Arg Asn Glu Ile Phe Ile
 405 410 415
 Leu Ser Arg Ala Gly Tyr Ala Gly Ile Gln Arg Tyr Ala Phe Ile Trp
 420 425 430
 Thr Gly Asp Asn Thr Pro Ser Trp Asp Asp Leu Lys Leu Gln Leu Gln
 435 440 445
 Leu Val Leu Gly Leu Ser Ile Ser Gly Val Pro Phe Val Gly Cys Asp
 450 455 460
 Ile Gly Gly Phe Gln Gly Arg Asn Phe Ala Glu Ile Asp Asn Ser Met

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```

465      470      475      480
Asp Leu Leu Val Lys Tyr Tyr Ala Leu Ala Leu Phe Phe Pro Phe Tyr
      485      490      495
Arg Ser His Lys Ala Thr Asp Gly Ile Asp Thr Glu Pro Val Phe Leu
      500      505      510
Pro Asp Tyr Tyr Lys Glu Lys Val Lys Glu Ile Val Glu Leu Arg Tyr
      515      520      525
Lys Phe Leu Pro Tyr Ile Tyr Ser Leu Ala Leu Glu Ala Ser Glu Lys
      530      535      540
Gly His Pro Val Ile Arg Pro Leu Phe Tyr Glu Phe Gln Asp Asp Asp
      545      550      555      560
Asp Met Tyr Arg Ile Glu Asp Glu Tyr Met Val Gly Lys Tyr Leu Leu
      565      570      575
Tyr Ala Pro Ile Val Ser Lys Glu Glu Ser Arg Leu Val Thr Leu Pro
      580      585      590
Arg Gly Lys Trp Tyr Asn Tyr Trp Asn Gly Glu Ile Ile Asn Gly Lys
      595      600      605
Ser Val Val Lys Ser Thr His Glu Leu Pro Ile Tyr Leu Arg Glu Gly
      610      615      620
Ser Ile Ile Pro Leu Glu Gly Asp Glu Leu Ile Val Tyr Gly Glu Thr
      625      630      635      640
Ser Phe Lys Arg Tyr Asp Asn Ala Glu Ile Thr Ser Ser Ser Asn Glu
      645      650      655
Ile Lys Phe Ser Arg Glu Ile Tyr Val Ser Lys Leu Thr Ile Thr Ser
      660      665      670
Glu Lys Pro Val Ser Lys Ile Ile Val Asp Asp Ser Lys Glu Ile Gln
      675      680      685
Val Glu Lys Thr Met Gln Asn Thr Tyr Val Ala Lys Ile Asn Gln Lys
      690      695      700
Ile Arg Gly Lys Ile Asn Leu Glu
      705      710

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<210> 28

<211> 469

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 28

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Met Arg Val Leu Leu Val Ala Leu Ala Leu Leu Ala Leu Ala Ala Ser
1      5      10      15
Ala Thr Ser Met Ala Glu Phe Phe Pro Glu Ile Pro Lys Ile Gln Phe
      20      25      30
Glu Gly Lys Glu Ser Thr Asn Pro Leu Ala Phe Arg Phe Tyr Asp Pro
      35      40      45
Asn Glu Val Ile Asp Gly Lys Pro Leu Lys Asp His Leu Lys Phe Ser
      50      55      60
Val Ala Phe Trp His Thr Phe Val Asn Glu Gly Arg Asp Pro Phe Gly
      65      70      75      80
Asp Pro Thr Ala Glu Arg Pro Trp Asn Arg Phe Ser Asp Pro Met Asp
      85      90      95
Lys Ala Phe Ala Arg Val Asp Ala Leu Phe Glu Phe Cys Glu Lys Leu
      100      105      110
Asn Ile Glu Tyr Phe Cys Phe His Asp Arg Asp Ile Ala Pro Glu Gly
      115      120      125
Lys Thr Leu Arg Glu Thr Asn Lys Ile Leu Asp Lys Val Val Glu Arg
      130      135      140
Ile Lys Glu Arg Met Lys Asp Ser Asn Val Lys Leu Leu Trp Gly Thr
      145      150      155      160
Ala Asn Leu Phe Ser His Pro Arg Tyr Met His Gly Ala Ala Thr Thr

```

60110USPCT1 Corrected SEQ LIST 2-2007.txt

Cys Ser Ala Asp Val Phe Ala Tyr Ala Ala Ala Gln Val Lys Lys Ala
 165 170 175
 180 185 190
 Leu Glu Ile Thr Lys Glu Leu Gly Gly Glu Gly Tyr Val Phe Trp Gly
 195 200 205
 Gly Arg Glu Gly Tyr Glu Thr Leu Leu Asn Thr Asp Leu Gly Leu Glu
 210 215 220
 Leu Glu Asn Leu Ala Arg Phe Leu Arg Met Ala Val Glu Tyr Ala Lys
 225 230 235 240
 Lys Ile Gly Phe Thr Gly Gln Phe Leu Ile Glu Pro Lys Pro Lys Glu
 245 250 255
 Pro Thr Lys His Gln Tyr Asp Phe Asp Val Ala Thr Ala Tyr Ala Phe
 260 265 270
 Leu Lys Asn His Gly Leu Asp Glu Tyr Phe Lys Phe Asn Ile Glu Ala
 275 280 285
 Asn His Ala Thr Leu Ala Gly His Thr Phe Gln His Glu Leu Arg Met
 290 295 300
 Ala Arg Ile Leu Gly Lys Leu Gly Ser Ile Asp Ala Asn Gln Gly Asp
 305 310 315 320
 Leu Leu Leu Gly Trp Asp Thr Asp Gln Phe Pro Thr Asn Ile Tyr Asp
 325 330 335
 Thr Thr Leu Ala Met Tyr Glu Val Ile Lys Ala Gly Gly Phe Thr Lys
 340 345 350
 Gly Gly Leu Asn Phe Asp Ala Lys Val Arg Arg Ala Ser Tyr Lys Val
 355 360 365
 Glu Asp Leu Phe Ile Gly His Ile Ala Gly Met Asp Thr Phe Ala Leu
 370 375 380
 Gly Phe Lys Ile Ala Tyr Lys Leu Ala Lys Asp Gly Val Phe Asp Lys
 385 390 395 400
 Phe Ile Glu Glu Lys Tyr Arg Ser Phe Lys Glu Gly Ile Gly Lys Glu
 405 410 415
 Ile Val Glu Gly Lys Thr Asp Phe Glu Lys Leu Glu Glu Tyr Ile Ile
 420 425 430
 Asp Lys Glu Asp Ile Glu Leu Pro Ser Gly Lys Gln Glu Tyr Leu Glu
 435 440 445
 Ser Leu Leu Asn Ser Tyr Ile Val Lys Thr Ile Ala Glu Leu Arg Ser
 450 455 460
 Glu Lys Asp Glu Leu
 465

<210> 29

<211> 469

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 29

Met Arg Val Leu Leu Val Ala Leu Ala Leu Leu Ala Leu Ala Ala Ser
 1 5 10 15
 Ala Thr Ser Met Ala Glu Phe Phe Pro Glu Ile Pro Lys Val Gln Phe
 20 25 30
 Glu Gly Lys Glu Ser Thr Asn Pro Leu Ala Phe Lys Phe Tyr Asp Pro
 35 40 45
 Glu Glu Ile Ile Asp Gly Lys Pro Leu Lys Asp His Leu Lys Phe Ser
 50 55 60
 Val Ala Phe Trp His Thr Phe Val Asn Glu Gly Arg Asp Pro Phe Gly
 65 70 75 80
 Asp Pro Thr Ala Asp Arg Pro Trp Asn Arg Tyr Thr Asp Pro Met Asp
 85 90 95
 Lys Ala Phe Ala Arg Val Asp Ala Leu Phe Glu Phe Cys Glu Lys Leu

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Asn Ile Glu Tyr Phe Cys Phe His Asp Arg Asp Ile Ala Pro Glu Gly
 100 105 110
 Lys Thr Leu Arg Glu Thr Asn Lys Ile Leu Asp Lys Val Val Glu Arg
 115 120 125
 Ile Lys Glu Arg Met Lys Asp Ser Asn Val Lys Leu Leu Trp Gly Thr
 130 135 140
 145 Ala Asn Leu Phe Ser His Pro Arg Tyr Met His Gly Ala Ala Thr Thr
 150 155 160
 Cys Ser Ala Asp Val Phe Ala Tyr Ala Ala Ala Gln Val Lys Lys Ala
 165 170 175
 Leu Glu Ile Thr Lys Glu Leu Gly Gly Glu Gly Tyr Val Phe Trp Gly
 180 185 190
 Gly Arg Glu Gly Tyr Glu Thr Leu Leu Asn Thr Asp Leu Gly Phe Glu
 195 200 205
 Leu Glu Asn Leu Ala Arg Phe Leu Arg Met Ala Val Asp Tyr Ala Lys
 210 215 220
 225 Arg Ile Gly Phe Thr Gly Gln Phe Leu Ile Glu Pro Lys Pro Lys Glu
 230 235 240
 Pro Thr Lys His Gln Tyr Asp Phe Asp Val Ala Thr Ala Tyr Ala Phe
 245 250 255
 Leu Lys Ser His Gly Leu Asp Glu Tyr Phe Lys Phe Asn Ile Glu Ala
 260 265 270
 Asn His Ala Thr Leu Ala Gly His Thr Phe Gln His Glu Leu Arg Met
 275 280 285
 Ala Arg Ile Leu Gly Lys Leu Gly Ser Ile Asp Ala Asn Gln Gly Asp
 290 295 300
 305 Leu Leu Leu Gly Trp Asp Thr Asp Gln Phe Pro Thr Asn Val Tyr Asp
 310 315 320
 Thr Thr Leu Ala Met Tyr Glu Val Ile Lys Ala Gly Gly Phe Thr Lys
 325 330 335
 Gly Gly Leu Asn Phe Asp Ala Lys Val Arg Arg Ala Ser Tyr Lys Val
 340 345 350
 Glu Asp Leu Phe Ile Gly His Ile Ala Gly Met Asp Thr Phe Ala Leu
 355 360 365
 Gly Phe Lys Val Ala Tyr Lys Leu Val Lys Asp Gly Val Leu Asp Lys
 370 375 380
 385 Phe Ile Glu Glu Lys Tyr Arg Ser Phe Arg Glu Gly Ile Gly Arg Asp
 390 395 400
 Ile Val Glu Gly Lys Val Asp Phe Glu Lys Leu Glu Glu Tyr Ile Ile
 405 410 415
 Asp Lys Glu Thr Ile Glu Leu Pro Ser Gly Lys Gln Glu Tyr Leu Glu
 420 425 430
 Ser Leu Ile Asn Ser Tyr Ile Val Lys Thr Ile Leu Glu Leu Arg Ser
 435 440 445
 450 Glu Lys Asp Glu Leu
 455 460
 465

<210> 30

<211> 463

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 30

Met Arg Val Leu Leu Val Ala Leu Ala Leu Leu Ala Leu Ala Ala Ser
 1 5 10 15
 Ala Thr Ser Met Ala Glu Phe Phe Pro Glu Ile Pro Lys Val Gln Phe
 20 25 30
 Glu Gly Lys Glu Ser Thr Asn Pro Leu Ala Phe Lys Phe Tyr Asp Pro

60110USPCT1 Corrected SEQ LIST 2-2007.txt

35 40 45
 Glu Glu Ile Ile Asp Gly Lys Pro Leu Lys Asp His Leu Lys Phe Ser
 50 55 60
 Val Ala Phe Trp His Thr Phe Val Asn Glu Gly Arg Asp Pro Phe Gly
 65 70 75 80
 Asp Pro Thr Ala Asp Arg Pro Trp Asn Arg Tyr Thr Asp Pro Met Asp
 85 90 95
 Lys Ala Phe Ala Arg Val Asp Ala Leu Phe Glu Phe Cys Glu Lys Leu
 100 105 110
 Asn Ile Glu Tyr Phe Cys Phe His Asp Arg Asp Ile Ala Pro Glu Gly
 115 120 125
 Lys Thr Leu Arg Glu Thr Asn Lys Ile Leu Asp Lys Val Val Glu Arg
 130 135 140
 Ile Lys Glu Arg Met Lys Asp Ser Asn Val Lys Leu Leu Trp Gly Thr
 145 150 155 160
 Ala Asn Leu Phe Ser His Pro Arg Tyr Met His Gly Ala Ala Thr Thr
 165 170 175
 Cys Ser Ala Asp Val Phe Ala Tyr Ala Ala Ala Gln Val Lys Lys Ala
 180 185 190
 Leu Glu Ile Thr Lys Glu Leu Gly Gly Glu Gly Tyr Val Phe Trp Gly
 195 200 205
 Gly Arg Glu Gly Tyr Glu Thr Leu Leu Asn Thr Asp Leu Gly Phe Glu
 210 215 220
 Leu Glu Asn Leu Ala Arg Phe Leu Arg Met Ala Val Asp Tyr Ala Lys
 225 230 235 240
 Arg Ile Gly Phe Thr Gly Gln Phe Leu Ile Glu Pro Lys Pro Lys Glu
 245 250 255
 Pro Thr Lys His Gln Tyr Asp Phe Asp Val Ala Thr Ala Tyr Ala Phe
 260 265 270
 Leu Lys Ser His Gly Leu Asp Glu Tyr Phe Lys Phe Asn Ile Glu Ala
 275 280 285
 Asn His Ala Thr Leu Ala Gly His Thr Phe Gln His Glu Leu Arg Met
 290 295 300
 Ala Arg Ile Leu Gly Lys Leu Gly Ser Ile Asp Ala Asn Gln Gly Asp
 305 310 315 320
 Leu Leu Leu Gly Trp Asp Thr Asp Gln Phe Pro Thr Asn Val Tyr Asp
 325 330 335
 Thr Thr Leu Ala Met Tyr Glu Val Ile Lys Ala Gly Gly Phe Thr Lys
 340 345 350
 Gly Gly Leu Asn Phe Asp Ala Lys Val Arg Arg Ala Ser Tyr Lys Val
 355 360 365
 Glu Asp Leu Phe Ile Gly His Ile Ala Gly Met Asp Thr Phe Ala Leu
 370 375 380
 Gly Phe Lys Val Ala Tyr Lys Leu Val Lys Asp Gly Val Leu Asp Lys
 385 390 395 400
 Phe Ile Glu Glu Lys Tyr Arg Ser Phe Arg Glu Gly Ile Gly Arg Asp
 405 410 415
 Ile Val Glu Gly Lys Val Asp Phe Glu Lys Leu Glu Glu Tyr Ile Ile
 420 425 430
 Asp Lys Glu Thr Ile Glu Leu Pro Ser Gly Lys Gln Glu Tyr Leu Glu
 435 440 445
 Ser Leu Ile Asn Ser Tyr Ile Val Lys Thr Ile Leu Glu Leu Arg
 450 455 460

<210> 31

<211> 25

<212> PRT

<213> Artificial sequence

<220>

<223> synthetic

60110USPCT1 Corrected SEQ LIST 2-2007.txt

<400> 31

Met Gly Lys Asn Gly Asn Leu Cys Cys Phe Ser Leu Leu Leu Leu Leu
 1 5 10 15
 Leu Ala Gly Leu Ala Ser Gly His Gln
 20 25

<210> 32

<211> 30

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 32

Met Gly Phe Val Leu Phe Ser Gln Leu Pro Ser Phe Leu Leu Val Ser
 1 5 10 15
 Thr Leu Leu Leu Phe Leu Val Ile Ser His Ser Cys Arg Ala
 20 25 30

<210> 33

<211> 460

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 33

Met Arg Val Leu Leu Val Ala Leu Ala Leu Leu Ala Leu Ala Ala Ser
 1 5 10 15
 Ala Thr Ser Ala Lys Tyr Leu Glu Leu Glu Glu Gly Gly Val Ile Met
 20 25 30
 Gln Ala Phe Tyr Trp Asp Val Pro Ser Gly Gly Ile Trp Trp Asp Thr
 35 40 45
 Ile Arg Gln Lys Ile Pro Glu Tyr Trp Tyr Asp Ala Gly Ile Ser Ala Ile
 50 55 60
 Trp Ile Pro Pro Ala Ser Lys Gly Met Ser Gly Gly Tyr Ser Met Gly
 65 70 75 80
 Tyr Asp Pro Tyr Asp Tyr Phe Asp Leu Gly Glu Tyr Tyr Gln Lys Gly
 85 90 95
 Thr Val Glu Thr Arg Phe Gly Ser Lys Gln Glu Leu Ile Asn Met Ile
 100 105 110
 Asn Thr Ala His Ala Tyr Gly Ile Lys Val Ile Ala Asp Ile Val Ile
 115 120 125
 Asn His Arg Ala Gly Gly Asp Leu Glu Trp Asn Pro Phe Val Gly Asp
 130 135 140
 Tyr Thr Trp Thr Asp Phe Ser Lys Val Ala Ser Gly Lys Tyr Thr Ala
 145 150 155 160
 Asn Tyr Leu Asp Phe His Pro Asn Glu Leu His Ala Gly Asp Ser Gly
 165 170 175
 Thr Phe Gly Gly Tyr Pro Asp Ile Cys His Asp Lys Ser Trp Asp Gln
 180 185 190
 Tyr Trp Leu Trp Ala Ser Gln Glu Ser Tyr Ala Ala Tyr Leu Arg Ser
 195 200 205
 Ile Gly Ile Asp Ala Trp Arg Phe Asp Tyr Val Lys Gly Tyr Gly Ala
 210 215 220
 Trp Val Val Lys Asp Trp Leu Asn Trp Trp Gly Gly Trp Ala Val Gly
 225 230 235 240
 Glu Tyr Trp Asp Thr Asn Val Asp Ala Leu Leu Asn Trp Ala Tyr Ser
 245 250 255

60110USPCT1 Corrected SEQ LIST 2-2007.txt

Ser Gly Ala Lys Val Phe Asp Phe Pro Leu Tyr Tyr Lys Met Asp Ala
 260 265 270
 Ala Phe Asp Asn Lys Asn Ile Pro Ala Leu Val Glu Ala Leu Lys Asn
 275 280 285
 Gly Gly Thr Val Val Ser Arg Asp Pro Phe Lys Ala Val Thr Phe Val
 290 295 300
 Ala Asn His Asp Thr Asp Ile Ile Trp Asn Lys Tyr Pro Ala Tyr Ala
 305 310 315 320
 Phe Ile Leu Thr Tyr Glu Gly Gln Pro Thr Ile Phe Tyr Arg Asp Tyr
 325 330 335
 Glu Glu Trp Leu Asn Lys Asp Lys Leu Lys Asn Leu Ile Trp Ile His
 340 345 350
 Asp Asn Leu Ala Gly Gly Ser Thr Ser Ile Val Tyr Tyr Asp Ser Asp
 355 360 365
 Glu Met Ile Phe Val Arg Asn Gly Tyr Gly Ser Lys Pro Gly Leu Ile
 370 375 380
 Thr Tyr Ile Asn Leu Gly Ser Ser Lys Val Gly Arg Trp Val Tyr Val
 385 390 395 400
 Pro Lys Phe Ala Gly Ala Cys Ile His Glu Tyr Thr Gly Asn Leu Gly
 405 410 415
 Gly Trp Val Asp Lys Tyr Val Tyr Ser Gly Trp Val Tyr Leu Glu
 420 425 430
 Ala Pro Ala Tyr Asp Pro Ala Asn Gly Gln Tyr Gly Tyr Ser Val Trp
 435 440 445
 Ser Tyr Cys Gly Val Gly Ser Glu Lys Asp Glu Leu
 450 455 460

<210> 34

<211> 825

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 34

Met Arg Val Leu Leu Val Ala Leu Ala Leu Leu Ala Leu Ala Ala Ser
 1 5 10 15
 Ala Thr Ser Ala Gly His Trp Tyr Lys His Gln Arg Ala Tyr Gln Phe
 20 25 30
 Thr Gly Glu Asp Asp Phe Gly Lys Val Ala Val Val Lys Leu Pro Met
 35 40 45
 Asp Leu Thr Lys Val Gly Ile Ile Val Arg Leu Asn Glu Trp Gln Ala
 50 55 60
 Lys Asp Val Ala Lys Asp Arg Phe Ile Glu Ile Lys Asp Gly Lys Ala
 65 70 75 80
 Glu Val Trp Ile Leu Gln Gly Val Glu Glu Ile Phe Tyr Glu Lys Pro
 85 90 95
 Asp Thr Ser Pro Arg Ile Phe Phe Ala Gln Ala Arg Ser Asn Lys Val
 100 105 110
 Ile Glu Ala Phe Leu Thr Asn Pro Val Asp Thr Lys Lys Lys Glu Leu
 115 120 125
 Phe Lys Val Thr Val Asp Gly Lys Glu Ile Pro Val Ser Arg Val Glu
 130 135 140
 Lys Ala Asp Pro Thr Asp Ile Asp Val Thr Asn Tyr Val Arg Ile Val
 145 150 155 160
 Leu Ser Glu Ser Leu Lys Glu Glu Asp Leu Arg Lys Asp Val Glu Leu
 165 170 175
 Ile Ile Glu Gly Tyr Lys Pro Ala Arg Val Ile Met Met Glu Ile Leu
 180 185 190
 Asp Asp Tyr Tyr Tyr Asp Gly Glu Leu Gly Ala Val Tyr Ser Pro Glu
 195 200 205

60110USPCT1 Corrected SEQ LIST 2-2007.txt

Lys	Thr	Ile	Phe	Arg	Val	Trp	Ser	Pro	Val	Ser	Lys	Trp	Val	Lys	Val
210						215				220					
Leu	Leu	Phe	Lys	Asn	Gly	Glu	Asp	Thr	Glu	Pro	Tyr	Gln	Val	Val	Asn
225					230					235					240
Met	Glu	Tyr	Lys	Gly	Asn	Gly	Val	Trp	Glu	Ala	Val	Val	Glu	Gly	Asp
				245					250					255	
Leu	Asp	Gly	Val	Phe	Tyr	Leu	Tyr	Gln	Leu	Glu	Asn	Tyr	Gly	Lys	Ile
			260					265					270		
Arg	Thr	Thr	Val	Asp	Pro	Tyr	Ser	Lys	Ala	Val	Tyr	Ala	Asn	Asn	Gln
		275					280					285			
Glu	Ser	Ala	Val	Val	Asn	Leu	Ala	Arg	Thr	Asn	Pro	Glu	Gly	Trp	Glu
	290				295					300					
Asn	Asp	Arg	Gly	Pro	Lys	Ile	Glu	Gly	Tyr	Glu	Asp	Ala	Ile	Ile	Tyr
305					310					315					320
Glu	Ile	His	Ile	Ala	Asp	Ile	Thr	Gly	Leu	Glu	Asn	Ser	Gly	Val	Lys
				325					330					335	
Asn	Lys	Gly	Leu	Tyr	Leu	Gly	Leu	Thr	Glu	Glu	Asn	Thr	Lys	Ala	Pro
			340					345					350		
Gly	Gly	Val	Thr	Thr	Gly	Leu	Ser	His	Leu	Val	Glu	Leu	Gly	Val	Thr
		355					360					365			
His	Val	His	Ile	Leu	Pro	Phe	Phe	Asp	Phe	Tyr	Thr	Gly	Asp	Glu	Leu
	370					375					380				
Asp	Lys	Asp	Phe	Glu	Lys	Tyr	Tyr	Asn	Trp	Gly	Tyr	Asp	Pro	Tyr	Leu
385					390					395					400
Phe	Met	Val	Pro	Glu	Gly	Arg	Tyr	Ser	Thr	Asp	Pro	Lys	Asn	Pro	His
				405					410					415	
Thr	Arg	Ile	Arg	Glu	Val	Lys	Glu	Met	Val	Lys	Ala	Leu	His	Lys	His
			420					425					430		
Gly	Ile	Gly	Val	Ile	Met	Asp	Met	Val	Phe	Pro	His	Thr	Tyr	Gly	Ile
		435				440						445			
Gly	Glu	Leu	Ser	Ala	Phe	Asp	Gln	Thr	Val	Pro	Tyr	Tyr	Phe	Tyr	Arg
	450					455				460					
Ile	Asp	Lys	Thr	Gly	Ala	Tyr	Leu	Asn	Glu	Ser	Gly	Cys	Gly	Asn	Val
465					470					475					480
Ile	Ala	Ser	Glu	Arg	Pro	Met	Met	Arg	Lys	Phe	Ile	Val	Asp	Thr	Val
				485					490					495	
Thr	Tyr	Trp	Val	Lys	Glu	Tyr	His	Ile	Asp	Gly	Phe	Arg	Phe	Asp	Gln
			500					505					510		
Met	Gly	Leu	Ile	Asp	Lys	Lys	Thr	Met	Leu	Glu	Val	Glu	Arg	Ala	Leu
		515					520					525			
His	Lys	Ile	Asp	Pro	Thr	Ile	Ile	Leu	Tyr	Gly	Glu	Pro	Trp	Gly	Gly
	530					535					540				
Trp	Gly	Ala	Pro	Ile	Arg	Phe	Gly	Lys	Ser	Asp	Val	Ala	Gly	Thr	His
545					550					555					560
Val	Ala	Ala	Phe	Asn	Asp	Glu	Phe	Arg	Asp	Ala	Ile	Arg	Gly	Ser	Val
				565					570					575	
Phe	Asn	Pro	Ser	Val	Lys	Gly	Phe	Val	Met	Gly	Gly	Tyr	Gly	Lys	Glu
			580					585					590		
Thr	Lys	Ile	Lys	Arg	Gly	Val	Val	Gly	Ser	Ile	Asn	Tyr	Asp	Gly	Lys
		595					600					605			
Leu	Ile	Lys	Ser	Phe	Ala	Leu	Asp	Pro	Glu	Glu	Thr	Ile	Asn	Tyr	Ala
	610					615					620				
Ala	Cys	His	Asp	Asn	His	Thr	Leu	Trp	Asp	Lys	Asn	Tyr	Leu	Ala	Ala
625					630					635					640
Lys	Ala	Asp	Lys	Lys	Lys	Glu	Trp	Thr	Glu	Glu	Glu	Leu	Lys	Asn	Ala
				645					650					655	
Gln	Lys	Leu	Ala	Gly	Ala	Ile	Leu	Leu	Thr	Ser	Gln	Gly	Val	Pro	Phe
			660					665					670		
Leu	His	Gly	Gly	Gln	Asp	Phe	Cys	Arg	Thr	Thr	Asn	Phe	Asn	Asp	Asn
		675					680					685			
Ser	Tyr	Asn	Ala	Pro	Ile	Ser	Ile	Asn	Gly	Phe	Asp	Tyr	Glu	Arg	Lys
	690					695					700				
Leu	Gln	Phe	Ile	Asp	Val	Phe	Asn	Tyr	His	Lys	Gly	Leu	Ile	Lys	Leu

60110USPCT1 Corrected SEQ LIST 2-2007.txt

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705          710          715          720
Arg Lys Glu His Pro Ala Phe Arg Leu Lys Asn Ala Glu Glu Ile Lys
          725          730          735
Lys His Leu Glu Phe Leu Pro Gly Gly Arg Arg Ile Val Ala Phe Met
          740          745          750
Leu Lys Asp His Ala Gly Gly Asp Pro Trp Lys Asp Ile Val Val Ile
          755          760          765
Tyr Asn Gly Asn Leu Glu Lys Thr Thr Tyr Lys Leu Pro Glu Gly Lys
          770          775          780
Trp Asn Val Val Val Asn Ser Gln Lys Ala Gly Thr Glu Val Ile Glu
785          790          795          800
Thr Val Glu Gly Thr Ile Glu Leu Asp Pro Leu Ser Ala Tyr Val Leu
          805          810          815
Tyr Arg Glu Ser Glu Lys Asp Glu Leu
          820          825

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<210> 35

<211> 460

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 35

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Met Arg Val Leu Leu Val Ala Leu Ala Leu Leu Ala Leu Ala Ala Ser
1          5          10          15
Ala Thr Ser Ala Lys Tyr Leu Glu Leu Glu Glu Gly Gly Val Ile Met
          20          25          30
Gln Ala Phe Tyr Trp Asp Val Pro Ser Gly Gly Ile Trp Trp Asp Thr
          35          40          45
Ile Arg Gln Lys Ile Pro Glu Trp Tyr Asp Ala Gly Ile Ser Ala Ile
          50          55          60
Trp Ile Pro Pro Ala Ser Lys Gly Met Ser Gly Gly Tyr Ser Met Gly
65          70          75          80
Tyr Asp Pro Tyr Asp Tyr Phe Asp Leu Gly Glu Tyr Tyr Gln Lys Gly
          85          90          95
Thr Val Glu Thr Arg Phe Gly Ser Lys Gln Glu Leu Ile Asn Met Ile
          100          105          110
Asn Thr Ala His Ala Tyr Gly Ile Lys Val Ile Ala Asp Ile Val Ile
          115          120          125
Asn His Arg Ala Gly Gly Asp Leu Glu Trp Asn Pro Phe Val Gly Asp
          130          135          140
Tyr Thr Trp Thr Asp Phe Ser Lys Val Ala Ser Gly Lys Tyr Thr Ala
145          150          155          160
Asn Tyr Leu Asp Phe His Pro Asn Glu Leu His Ala Gly Asp Ser Gly
          165          170          175
Thr Phe Gly Gly Tyr Pro Asp Ile Cys His Asp Lys Ser Trp Asp Gln
          180          185          190
Tyr Trp Leu Trp Ala Ser Gln Glu Ser Tyr Ala Ala Tyr Leu Arg Ser
          195          200          205
Ile Gly Ile Asp Ala Trp Arg Phe Asp Tyr Val Lys Gly Tyr Gly Ala
210          215          220
Trp Val Val Lys Asp Trp Leu Asn Trp Trp Gly Gly Trp Ala Val Gly
225          230          235          240
Glu Tyr Trp Asp Thr Asn Val Asp Ala Leu Leu Asn Trp Ala Tyr Ser
          245          250          255
Ser Gly Ala Lys Val Phe Asp Phe Pro Leu Tyr Tyr Lys Met Asp Ala
          260          265          270
Ala Phe Asp Asn Lys Asn Ile Pro Ala Leu Val Glu Ala Leu Lys Asn
          275          280          285
Gly Gly Thr Val Val Ser Arg Asp Pro Phe Lys Ala Val Thr Phe Val

```

60110USPCT1 Corrected SEQ LIST 2-2007.txt

290	295	300																	
Ala Asn His Asp Thr	Asp Ile Ile Trp Asn Lys Tyr	Pro Ala Tyr Ala																	
305	310	315																	
Phe Ile Leu Thr Tyr	Glu Gly Gln Pro Thr Ile Phe Tyr Arg Asp	Tyr																	
	325	330																	
Glu Glu Trp Leu Asn Lys Asp Lys	Leu Lys Asn Leu Ile Trp Ile His																		
	340	345																	
Asp Asn Leu Ala Gly Gly Ser Thr	Ser Ile Val Tyr Tyr Asp Ser Asp																		
	355	360																	
Glu Met Ile Phe Val Arg Asn Gly Tyr Gly Ser Lys	Pro Gly Leu Ile																		
	370	375																	
Thr Tyr Ile Asn Leu Gly Ser Ser Lys Val Gly Arg Trp Val Tyr Val																			
385	390	395																	
Pro Lys Phe Ala Gly Ala Cys Ile His Glu Tyr Thr Gly Asn Leu Gly																			
	405	410																	
Gly Trp Val Asp Lys Tyr Val Tyr Ser Ser Gly Trp Val Tyr Leu Glu																			
	420	425																	
Ala Pro Ala Tyr Asp Pro Ala Asn Gly Gln Tyr Gly Tyr Ser Val Trp																			
	435	440																	
Ser Tyr Cys Gly Val Gly Ser Glu Lys Asp Glu Leu																			
450	455	460																	

<210> 36
 <211> 718
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 36																			
Met Arg Val Leu Leu Val Ala Leu Ala Leu Leu Ala Leu Ala Ala Ser																			
1	5	10	15																
Ala Thr Ser Met Glu Thr Ile Lys Ile Tyr Glu Asn Lys Gly Val Tyr																			
	20	25	30																
Lys Val Val Ile Gly Glu Pro Phe Pro Pro Ile Glu Phe Pro Leu Glu																			
	35	40	45																
Gln Lys Ile Ser Ser Asn Lys Ser Leu Ser Glu Leu Gly Leu Thr Ile																			
	50	55	60																
Val Gln Gln Gly Asn Lys Val Ile Val Glu Lys Ser Leu Asp Leu Lys																			
65	70	75	80																
Glu His Ile Ile Gly Leu Gly Glu Lys Ala Phe Glu Leu Asp Arg Lys																			
	85	90	95																
Arg Lys Arg Tyr Val Met Tyr Asn Val Asp Ala Gly Ala Tyr Lys Lys																			
	100	105	110																
Tyr Gln Asp Pro Leu Tyr Val Ser Ile Pro Leu Phe Ile Ser Val Lys																			
	115	120	125																
Asp Gly Val Ala Thr Gly Tyr Phe Phe Asn Ser Ala Ser Lys Val Ile																			
	130	135	140																
Phe Asp Val Gly Leu Glu Glu Tyr Asp Lys Val Ile Val Thr Ile Pro																			
145	150	155	160																
Glu Asp Ser Val Glu Phe Tyr Val Ile Glu Gly Pro Arg Ile Glu Asp																			
	165	170	175																
Val Leu Glu Lys Tyr Thr Glu Leu Thr Gly Lys Pro Phe Leu Pro Pro																			
	180	185	190																
Met Trp Ala Phe Gly Tyr Met Ile Ser Arg Tyr Ser Tyr Tyr Pro Gln																			
	195	200	205																
Asp Lys Val Val Glu Leu Val Asp Ile Met Gln Lys Glu Gly Phe Arg																			
	210	215	220																
Val Ala Gly Val Phe Leu Asp Ile His Tyr Met Asp Ser Tyr Lys Leu																			
225	230	235	240																
Phe Thr Trp His Pro Tyr Arg Phe Pro Glu Pro Lys Lys Leu Ile Asp																			

60110USPCT1 Corrected SEQ LIST 2-2007.txt

245 250 255
 Glu Leu His Lys Arg Asn Val Lys Leu Ile Thr Ile Val Asp His Gly
 260 265 270
 Ile Arg Val Asp Gln Asn Tyr Ser Pro Phe Leu Ser Gly Met Gly Lys
 275 280 285
 Phe Cys Glu Ile Glu Ser Gly Glu Leu Phe Val Gly Lys Met Trp Pro
 290 295 300
 Gly Thr Thr Val Tyr Pro Asp Phe Phe Arg Glu Asp Thr Arg Glu Trp
 305 310 315 320
 Trp Ala Gly Leu Ile Ser Glu Trp Leu Ser Gln Gly Val Asp Gly Ile
 325 330 335
 Trp Leu Asp Met Asn Glu Pro Thr Asp Phe Ser Arg Ala Ile Glu Ile
 340 345 350
 Arg Asp Val Leu Ser Ser Leu Pro Val Gln Phe Arg Asp Arg Leu
 355 360 365
 Val Thr Thr Phe Pro Asp Asn Val Val His Tyr Leu Arg Gly Lys Arg
 370 375 380
 Val Lys His Glu Lys Val Arg Asn Ala Tyr Pro Leu Tyr Glu Ala Met
 385 390 395 400
 Ala Thr Phe Lys Gly Phe Arg Thr Ser His Arg Asn Glu Ile Phe Ile
 405 410 415
 Leu Ser Arg Ala Gly Tyr Ala Gly Ile Gln Arg Tyr Ala Phe Ile Trp
 420 425 430
 Thr Gly Asp Asn Thr Pro Ser Trp Asp Asp Leu Lys Leu Gln Leu Gln
 435 440 445
 Leu Val Leu Gly Leu Ser Ile Ser Gly Val Pro Phe Val Gly Cys Asp
 450 455 460
 Ile Gly Gly Phe Gln Gly Arg Asn Phe Ala Glu Ile Asp Asn Ser Met
 465 470 475 480
 Asp Leu Leu Val Lys Tyr Tyr Ala Leu Ala Leu Phe Phe Pro Phe Tyr
 485 490 495
 Arg Ser His Lys Ala Thr Asp Gly Ile Asp Thr Glu Pro Val Phe Leu
 500 505 510
 Pro Asp Tyr Tyr Lys Glu Lys Val Lys Glu Ile Val Glu Leu Arg Tyr
 515 520 525
 Lys Phe Leu Pro Tyr Ile Tyr Ser Leu Ala Leu Glu Ala Ser Glu Lys
 530 535 540
 Gly His Pro Val Ile Arg Pro Leu Phe Tyr Glu Phe Gln Asp Asp Asp
 545 550 555 560
 Asp Met Tyr Arg Ile Glu Asp Glu Tyr Met Val Gly Lys Tyr Leu Leu
 565 570 575
 Tyr Ala Pro Ile Val Ser Lys Glu Glu Ser Arg Leu Val Thr Leu Pro
 580 585 590
 Arg Gly Lys Trp Tyr Asn Tyr Trp Asn Gly Glu Ile Ile Asn Gly Lys
 595 600 605
 Ser Val Val Lys Ser Thr His Glu Leu Pro Ile Tyr Leu Arg Glu Gly
 610 615 620
 Ser Ile Ile Pro Leu Glu Gly Asp Glu Leu Ile Val Tyr Gly Glu Thr
 625 630 635 640
 Ser Phe Lys Arg Tyr Asp Asn Ala Glu Ile Thr Ser Ser Ser Asn Glu
 645 650 655
 Ile Lys Phe Ser Arg Glu Ile Tyr Val Ser Lys Leu Thr Ile Thr Ser
 660 665 670
 Glu Lys Pro Val Ser Lys Ile Ile Val Asp Asp Ser Lys Glu Ile Gln
 675 680 685
 Val Glu Lys Thr Met Gln Asn Thr Tyr Val Ala Lys Ile Asn Gln Lys
 690 695 700
 Ile Arg Gly Lys Ile Asn Leu Glu Ser Glu Lys Asp Glu Leu
 705 710 715

<210> 37

<211> 1434

60110USPCT1 Corrected SEQ LIST 2-2007.txt

<212> DNA

<213> *Thermotoga maritima*

<400> 37

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atgaaagaaa cgcgtgctgc taaattcgaa cgccagcaca tggacagccc agatctgggt 60
accctgggtgc cagcggttc catggccgag ttcttcccgg agatcccga gatccagttc 120
gagggcaagg agtccaccaa cccgctcgcc ttccgcttct acgacccga cgaggtgata 180
gacggcaagc cgtcaagga ccacctcaag ttctccgtgg ccttctggca caccttcgtg 240
aacgagggcc gcgaccggt cggcgacccg accgcccagc gcccgaggaa ccgcttctcc 300
gacccgatgg acaaggcctt cgcccgcgtg gacgcccctt tcgagttctg cgagaagctc 360
aacatcgagt acttctgctt ccacgaccgc gacatcgccc cggagggcaa gaccctccgc 420
gagaccaaca agatcctcga caaggtgggt gagcgcatca aggagcgat gaaggactcc 480
aacgtgaagc tcctctgggg caccgccaac ctcttctccc acccgcgcta catgcacggc 540
gccgccacca cctgctccgc cgacgtgttc gcctacgccc ccgcccaggt gaagaaggcc 600
ctggagatca ccaaggagct gggcgcgag ggctacgtgt tctggggcgg ccgagggg 660
tacgagacc tcctcaacac cgacctcggc ctggagctgg agaacctcgc ccgcttctc 720
cgcatggccg tggagtacgc caagaagatc ggcttcaccg gccagttcct catcgagccg 780
aagccgaagg agccgacca gacacgtac gacttcgacg tggccaccgc ctacgccttc 840
ctcaagaacc acggcctcga cgagtacttc aagttcaaca tcgaggccaa ccacgccacc 900
ctcgccggcc acaccttcca gcacgagctg cgcatggccc gcatcctcgg caagctcggc 960
tccatcgagc ccaaccagg cgacctctc ctggctggg acaccgacca gttcccggcc 1020
aacatctacg acaccacct cgccatgtac gaggtgatca aggccggcgg cttaccaag 1080
ggcgccctca acttcgacgc caaggtgcgc cgccctcctt acaaggtgga ggacctcttc 1140
atcgccacca tcgcccggcat ggacaccttc gccctcggct tcaagatcgc ctacaagctc 1200
gccaaaggac gcgtgttcga caagttcatc gaggagaagt accgctcctt caaggagggc 1260
atcggaagg agatcgagg gggcaagacc gacttcgaga agctggagga gtacatcatc 1320
gacaaggagg acatcgagct gccgtccggc aagcaggagt acctggagtc cctcctcaac 1380
tcctacatcg tgaagaccat cgccgagctg cgctccgaga aggacgagct gtga 1434

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<210> 38

<211> 477

<212> PRT

<213> *Thermotoga maritima*

<400> 38

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Met Lys Glu Thr Ala Ala Lys Phe Glu Arg Gln His Met Asp Ser
1      5      10      15
Pro Asp Leu Gly Thr Leu Val Pro Arg Gly Ser Met Ala Glu Phe Phe
20     25     30
Pro Glu Ile Pro Lys Ile Gln Phe Glu Gly Lys Glu Ser Thr Asn Pro
35     40     45
Leu Ala Phe Arg Phe Tyr Asp Pro Asn Glu Val Ile Asp Gly Lys Pro
50     55     60
Leu Lys Asp His Leu Lys Phe Ser Val Ala Phe Trp His Thr Phe Val
65     70     75     80
Asn Glu Gly Arg Asp Pro Phe Gly Asp Pro Thr Ala Glu Arg Pro Trp
85     90     95
Asn Arg Phe Ser Asp Pro Met Asp Lys Ala Phe Ala Arg Val Asp Ala
100    105    110
Leu Phe Glu Phe Cys Glu Lys Leu Asn Ile Glu Tyr Phe Cys Phe His
115    120    125
Asp Arg Asp Ile Ala Pro Glu Gly Lys Thr Leu Arg Glu Thr Asn Lys
130    135    140
Ile Leu Asp Lys Val Val Glu Arg Ile Lys Glu Arg Met Lys Asp Ser
145    150    155    160
Asn Val Lys Leu Leu Trp Gly Thr Ala Asn Leu Phe Ser His Pro Arg
165    170    175
Tyr Met His Gly Ala Ala Thr Thr Cys Ser Ala Asp Val Phe Ala Tyr
180    185    190
Ala Ala Ala Gln Val Lys Lys Ala Leu Glu Ile Thr Lys Glu Leu Gly
195    200    205
Gly Glu Gly Tyr Val Phe Trp Gly Gly Arg Glu Gly Tyr Glu Thr Leu
210    215    220

```

60110USPCT1 Corrected SEQ LIST 2-2007.txt

Leu	Asn	Thr	Asp	Leu	Gly	Leu	Glu	Leu	Glu	Asn	Leu	Ala	Arg	Phe	Leu
225					230					235					240
Arg	Met	Ala	Val	Glu	Tyr	Ala	Lys	Lys	Ile	Gly	Phe	Thr	Gly	Gln	Phe
				245					250					255	
Leu	Ile	Glu	Pro	Lys	Pro	Lys	Glu	Pro	Thr	Lys	His	Gln	Tyr	Asp	Phe
			260					265					270		
Asp	Val	Ala	Thr	Ala	Tyr	Ala	Phe	Leu	Lys	Asn	His	Gly	Leu	Asp	Glu
		275					280					285			
Tyr	Phe	Lys	Phe	Asn	Ile	Glu	Ala	Asn	His	Ala	Thr	Leu	Ala	Gly	His
	290				295						300				
Thr	Phe	Gln	His	Glu	Leu	Arg	Met	Ala	Arg	Ile	Leu	Gly	Lys	Leu	Gly
305				310						315					320
Ser	Ile	Asp	Ala	Asn	Gln	Gly	Asp	Leu	Leu	Leu	Gly	Trp	Asp	Thr	Asp
				325				330						335	
Gln	Phe	Pro	Thr	Asn	Ile	Tyr	Asp	Thr	Leu	Ala	Met	Tyr	Glu	Val	
			340					345				350			
Ile	Lys	Ala	Gly	Gly	Phe	Thr	Lys	Gly	Gly	Leu	Asn	Phe	Asp	Ala	Lys
	355						360					365			
Val	Arg	Arg	Ala	Ser	Tyr	Lys	Val	Glu	Asp	Leu	Phe	Ile	Gly	His	Ile
	370				375						380				
Ala	Gly	Met	Asp	Thr	Phe	Ala	Leu	Gly	Phe	Lys	Ile	Ala	Tyr	Lys	Leu
385					390					395					400
Ala	Lys	Asp	Gly	Val	Phe	Asp	Lys	Phe	Ile	Glu	Glu	Lys	Tyr	Arg	Ser
			405					410						415	
Phe	Lys	Glu	Gly	Ile	Gly	Lys	Glu	Ile	Val	Glu	Gly	Lys	Thr	Asp	Phe
			420					425					430		
Glu	Lys	Leu	Glu	Glu	Tyr	Ile	Ile	Asp	Lys	Glu	Asp	Ile	Glu	Leu	Pro
		435				440						445			
Ser	Gly	Lys	Gln	Glu	Tyr	Leu	Glu	Ser	Leu	Leu	Asn	Ser	Tyr	Ile	Val
	450					455					460				
Lys	Thr	Ile	Ala	Glu	Leu	Arg	Ser	Glu	Lys	Asp	Glu	Leu			
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<210> 39
 <211> 1434
 <212> DNA
 <213> Thermotoga neapolitana

<400> 39

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gagggcaagg	agtcaccaa	cccgtcgcgc	ttcaagtctt	acgacccgga	ggagatcatc	180
gacggcaagc	cgctcaagga	ccacctcaag	ttcttcgtgg	ccttctggca	caccttcgtg	240
aacgagggcc	gcgacccgtt	cggcgacccg	accgcccacc	gcccgtggaa	ccgctacacc	300
gacccgatgg	acaaggcctt	cgcccgcgtg	gacgccctct	tcgagttctg	cgagaagctc	360
aacatcgagt	acttctgctt	ccacgaccgc	gacatcgccc	cggagggcaa	gaccctccgc	420
gagaccaaca	agatcctcga	caagggtggt	gagcgcacat	aggagcgcat	gaaggactcc	480
aacgtgaagc	tcctctgggg	caccgccaac	ctcttctccc	acccgcgcta	catgcacggc	540
gccgccacca	cctgctccgc	cgacgtgttc	gcctacgccg	ccgcccaggt	gaagaaggcc	600
ctggagatca	ccaaggagct	gggcggcgag	ggctacgtgt	tctggggcgg	ccgcgagggc	660
tacgagacct	tcctcaacac	cgacctcggc	ttcgagctgg	agaacctcgc	ccgcttcctc	720
cgcattggccg	tggactacgc	caagcgcac	ggcttcaccg	gccagttcct	catcgagccg	780
aagccgaagg	agccgaccaa	gcaccagtac	gacttcgacg	tggccaccgc	ctacgccttc	840
ctcaagtccc	acggcctcga	cgagtacttc	aagtccaaca	tcgaggccaa	ccacgccacc	900
ctcgcgggcc	acaccttcca	gcacgagctg	cgcattggccc	gcattcctcg	caagctcggc	960
tccatcgacg	ccaaccaggg	cgacctcctc	ctcggctggg	acaccgacca	gttcccagacc	1020
aacgtgtacg	acaccaccct	cgccatgtac	gaggtgatca	aggccggcgg	cttcaccaag	1080
ggcggcctca	acttcgacgc	caagggtgcg	cgcgcctcct	acaagggtga	ggacctcttc	1140
atcgggccaca	tcgcccggcat	ggacaccttc	gccctcggct	tcaagggtggc	ctacaagctc	1200
gtgaaggacg	cggtgctcga	caagttcatc	gaggagaagt	accgctcctt	ccgcgagggc	1260
atcggccgcg	acatcgtgga	gggcaagggt	gacttcgaga	agctggagga	gtacatcatc	1320
gacaaggaga	ccatcgagct	gccgtccggc	aagcaggagt	acctggagtc	cctcatcaac	1380

<210> 40
<211> 477
<212> PRT
<213> Thermotoga neapolitana

<400> 40
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20 25 30
Pro Glu Ile Pro Lys Val Gln Phe Glu Gly Lys Glu Ser Thr Asn Pro
35 40 45
Leu Ala Phe Lys Phe Tyr Asp Pro Glu Glu Ile Ile Asp Gly Lys Pro
50 55 60
Leu Lys Asp His Leu Lys Phe Ser Val Ala Phe Trp His Thr Phe Val
65 70 75 80
Asn Glu Gly Arg Asp Pro Phe Gly Asp Pro Thr Ala Asp Arg Pro Trp
85 90 95
Asn Arg Tyr Thr Asp Pro Met Asp Lys Ala Phe Ala Arg Val Asp Ala
100 105 110
Leu Phe Glu Phe Cys Glu Lys Leu Asn Ile Glu Tyr Phe Cys Phe His
115 120 125
Asp Arg Asp Ile Ala Pro Glu Gly Lys Thr Leu Arg Glu Thr Asn Lys
130 135 140
Ile Leu Asp Lys Val Val Glu Arg Ile Lys Glu Arg Met Lys Asp Ser
145 150 155 160
Asn Val Lys Leu Leu Trp Gly Thr Ala Asn Leu Phe Ser His Pro Arg
165 170 175
Tyr Met His Gly Ala Ala Thr Thr Cys Ser Ala Asp Val Phe Ala Tyr
180 185 190
Ala Ala Ala Gln Val Lys Lys Ala Leu Glu Ile Thr Lys Glu Leu Gly
195 200 205
Gly Glu Gly Tyr Val Phe Trp Gly Gly Arg Glu Gly Tyr Glu Thr Leu
210 215 220
Leu Asn Thr Asp Leu Gly Phe Glu Leu Glu Asn Leu Ala Arg Phe Leu
225 230 235 240
Arg Met Ala Val Asp Tyr Ala Lys Arg Ile Gly Phe Thr Gly Gln Phe
245 250 255
Leu Ile Glu Pro Lys Pro Lys Glu Pro Thr Lys His Gln Tyr Asp Phe
260 265 270
Asp Val Ala Thr Ala Tyr Ala Phe Leu Lys Ser His Gly Leu Asp Glu
275 280 285
Tyr Phe Lys Phe Asn Ile Glu Ala Asn His Ala Thr Leu Ala Gly His
290 295 300
Thr Phe Gln His Glu Leu Arg Met Ala Arg Ile Leu Gly Lys Leu Gly
305 310 315 320
Ser Ile Asp Ala Asn Gln Gly Asp Leu Leu Gly Trp Asp Thr Asp
325 330 335
Gln Phe Pro Thr Asn Val Tyr Asp Thr Thr Leu Ala Met Tyr Glu Val
340 345 350
Ile Lys Ala Gly Gly Phe Thr Lys Gly Gly Leu Asn Phe Asp Ala Lys
355 360 365
Val Arg Arg Ala Ser Tyr Lys Val Glu Asp Leu Phe Ile Gly His Ile
370 375 380
Ala Gly Met Asp Thr Phe Ala Leu Gly Phe Lys Val Ala Tyr Lys Leu
385 390 395 400
Val Lys Asp Gly Val Leu Asp Lys Phe Ile Glu Glu Lys Tyr Arg Ser
405 410 415
Phe Arg Glu Gly Ile Gly Arg Asp Ile Val Glu Gly Lys Val Asp Phe
420 425 430
Glu Lys Leu Glu Glu Tyr Ile Ile Asp Lys Glu Thr Ile Glu Leu Pro

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435 440 445
 Ser Gly Lys Gln Glu Tyr Leu Glu Ser Leu Ile Asn Ser Tyr Ile Val
 450 455 460
 Lys Thr Ile Leu Glu Leu Arg Ser Glu Lys Asp Glu Leu
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<210> 41
 <211> 1435
 <212> DNA
 <213> Thermotoga maritima

<400> 41
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 gagatcccga agatccagtt cgagggaag gagtccacca acccgctcgc ctcccgcttc 180
 tacgaccgga acgaggtgat cgacggcaag ccgctcaagg accacctcaa gttctccgtg 240
 gccttctggc acaccttcgt gaacgagggc cgcgaccggt tcggcgaccc gaccgcccag 300
 cggccgtgga accgcttctc cgacccgatg gacaaggcct tcgcccgcgt ggacgcccctc 360
 ttcgagttct gcgagaagct caacatcgag tacttctgct tccacgaccg cgacatcccc 420
 cggagggcaa gacctccgc gagaccaaca agatcctcga caagggtggt gagcgcatca 480
 aggagcgcat gaaggactcc aacgtgaagc tcctctgggg caccgccaac ctcttctccc 540
 acccgcgcta catgcacggc gccgccacca cctgctccgc cgacgtgttc gcctacgccg 600
 ccgcccaggt gaagaaggcc ctggagatca ccaaggagct gggcggcgag ggctacgtgt 660
 tctggggcgg ccgcgagggc tacgagaccc tcctcaacac cgacctcggc ctggagctgg 720
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 gccagttcct catcgagccg aagccgaagg agccgacca gcaccagtac gcttcgacgt 840
 ggccaccgcc tacgccttcc tcaagaacca cggcctcgac gagtacttca agttcaacat 900
 cgaggccaac cagccacccc tcgcccggca caccctccag cagagctgc gcatggccc 960
 catcctcggc aagctcggct ccacgacgc caaccagggc gacctcctcc tcggctggga 1020
 caccgaccag ttcccgaaca acatctacga caccaccctc gccatgtacg aggtgatcaa 1080
 ggccggcggc ttcaccaagg gcggcctcaa cttcgacgcc aaggtgcgcc gcgcctccta 1140
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 caagatgcc tacaagctcg ccaaggacgg cgtgttcgac aagttcatcg aggagaagta 1260
 ccgctccttc aaggagggca tcggcaagga gatcgtggag ggcaagaccg acttcgagaa 1320
 gctggaggag tacatcatcg acaaggagga catcgagctg ccgtccggca agcaggagta 1380
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<210> 42
 <211> 478
 <212> PRT
 <213> Thermotoga maritima

<400> 42
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 35 40 45
 Gly Lys Glu Ser Thr Asn Pro Leu Ala Phe Arg Phe Tyr Asp Pro Asn
 50 55 60
 Glu Val Ile Asp Gly Lys Pro Leu Lys Asp His Leu Lys Phe Ser Val
 65 70 75 80
 Ala Phe Trp His Thr Phe Val Asn Glu Gly Arg Asp Pro Phe Gly Asp
 85 90 95
 Pro Thr Ala Glu Arg Pro Trp Asn Arg Phe Ser Asp Pro Met Asp Lys
 100 105 110
 Ala Phe Ala Arg Val Asp Ala Leu Phe Glu Phe Cys Glu Lys Leu Asn
 115 120 125
 Ile Glu Tyr Phe Cys Phe His Asp Arg Asp Ile Ala Pro Glu Gly Lys
 130 135 140
 Thr Leu Arg Glu Thr Asn Lys Ile Leu Asp Lys Val Val Glu Arg Ile

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145		150		155		160
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165		170		175		180
Asn	Leu	Phe	Ser	His	Pro	Arg
185		190		195		200
Ser	Ala	Asp	Val	Phe	Ala	Tyr
205		210		215		220
Glu	Ile	Thr	Lys	Glu	Leu	Gly
225		230		235		240
Arg	Glu	Gly	Tyr	Glu	Thr	Leu
245		250		255		260
Glu	Asn	Leu	Ala	Arg	Phe	Leu
265		270		275		280
Ile	Gly	Phe	Thr	Gly	Gln	Phe
285		290		295		300
Thr	Lys	His	Gln	Tyr	Asp	Phe
305		310		315		320
Lys	Asn	His	Gly	Leu	Asp	Glu
325		330		335		340
His	Ala	Thr	Leu	Ala	Gly	His
345		350		355		360
Arg	Ile	Leu	Gly	Lys	Leu	Gly
365		370		375		380
Leu	Leu	Gly	Trp	Asp	Thr	Asp
385		390		395		400
Thr	Leu	Ala	Met	Tyr	Glu	Val
405		410		415		420
Gly	Leu	Asn	Phe	Asp	Ala	Lys
425		430		435		440
Asp	Leu	Phe	Ile	Gly	His	Ile
445		450		455		460
Phe	Lys	Ile	Ala	Tyr	Lys	Leu
465		470		475		
Ile	Glu	Glu	Lys	Tyr	Arg	Ser
Val	Glu	Gly	Lys	Thr	Asp	Phe
Lys	Glu	Asp	Ile	Glu	Leu	Pro
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<210> 43

<211> 1436

<212> DNA

<213> Thermotoga neapolitana

<400> 43

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gagatcccga	aggtgcagtt	cgagggcaag	gagtcaccca	acccgctcgc	cttcaagttc	180
tacgacccgg	aggagatcat	cgacggcaag	ccgctcaagg	accacctcaa	gttctccgtg	240
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cgcccgtgga	accgctacac	cgacccgatg	gacaaggcct	tcgcccgcgt	ggacgcccctc	360
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cggagggcaa	gaccctccgc	gagaccaaca	agatcctcga	caagggtggtg	gagcgcacatca	480
aggagcgcac	gaaggactcc	aacgtgaagc	tcctctgggg	caccgccaac	ctcttctccc	540
acccgcgcta	catgcacggc	gccgccacca	cctgctccgc	cgacgtgttc	gcctacgccg	600
ccgcccaggt	gaagaaggcc	ctggagatca	ccaaggagct	gggcggcgag	ggctacgtgt	660
tctggggcgc	ccgcgagggc	tacgagacct	tcctcaacac	cgacctcggc	ttcgagctgg	720
agaacctcgc	ccgcttcctc	cgcatggccg	tggactacgc	caagcgcatc	ggcttcaccg	780
gccagttcct	catcgagccg	aagccgaagg	agccgaccaa	gcaccagtac	gacttcgacg	840

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gcatcctcgg caagctcggc tccatcgacg ccaaccaggg cgacctctc ctcggctggg 1020
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aggccggcgg cttcaccaag ggcggcctca acttcgacgc caaggtgcgc cgcgcctcct 1140
acaaggtgga ggacctcttc atcggccaca tcggccggcat ggacaccttc gccctcggct 1200
tcaaggtggc ctacaagctc gtgaaggacg gcgtgctcga caagttcatc gaggagaagt 1260
accgctcctt ccgcgagggc atcggccgcg acatcggtga gggcaaggtg gacttcgaga 1320
agctggagga gtacatcatc gacaaggaga ccacgcgagc gccgtccggc aagcaggagt 1380
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<210> 44

<211> 478

<212> PRT

<213> Thermotoga neapolitana

<400> 44

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35     40     45
Gly Lys Glu Ser Thr Asn Pro Leu Ala Phe Lys Phe Tyr Asp Pro Glu
50     55     60
Glu Ile Ile Asp Gly Lys Pro Leu Lys Asp His Leu Lys Phe Ser Val
65     70     75     80
Ala Phe Trp His Thr Phe Val Asn Glu Gly Arg Asp Pro Phe Gly Asp
85     90     95
Pro Thr Ala Asp Arg Pro Trp Asn Arg Tyr Thr Asp Pro Met Asp Lys
100    105    110
Ala Phe Ala Arg Val Asp Ala Leu Phe Glu Phe Cys Glu Lys Leu Asn
115    120    125
Ile Glu Tyr Phe Cys Phe His Asp Arg Asp Ile Ala Pro Glu Gly Lys
130    135    140
Thr Leu Arg Glu Thr Asn Lys Ile Leu Asp Lys Val Val Glu Arg Ile
145    150    155    160
Lys Glu Arg Met Lys Asp Ser Asn Val Lys Leu Leu Trp Gly Thr Ala
165    170    175
Asn Leu Phe Ser His Pro Arg Tyr Met His Gly Ala Ala Thr Thr Cys
180    185    190
Ser Ala Asp Val Phe Ala Tyr Ala Ala Ala Gln Val Lys Lys Ala Leu
195    200    205
Glu Ile Thr Lys Glu Leu Gly Gly Glu Gly Tyr Val Phe Trp Gly Gly
210    215    220
Arg Glu Gly Tyr Glu Thr Leu Leu Asn Thr Asp Leu Gly Phe Glu Leu
225    230    235    240
Glu Asn Leu Ala Arg Phe Leu Arg Met Ala Val Asp Tyr Ala Lys Arg
245    250    255
Ile Gly Phe Thr Gly Gln Phe Leu Ile Glu Pro Lys Pro Lys Glu Pro
260    265    270
Thr Lys His Gln Tyr Asp Phe Asp Val Ala Thr Ala Tyr Ala Phe Leu
275    280    285
Lys Ser His Gly Leu Asp Glu Tyr Phe Lys Phe Asn Ile Glu Ala Asn
290    295    300
His Ala Thr Leu Ala Gly His Thr Phe Gln His Glu Leu Arg Met Ala
305    310    315    320
Arg Ile Leu Gly Lys Leu Gly Ser Ile Asp Ala Asn Gln Gly Asp Leu
325    330    335
Leu Leu Gly Trp Asp Thr Asp Gln Phe Pro Thr Asn Val Tyr Asp Thr
340    345    350
Thr Leu Ala Met Tyr Glu Val Ile Lys Ala Gly Gly Phe Thr Lys Gly
355    360    365

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Gly Leu Asn Phe Asp Ala Lys Val Arg Arg Ala Ser Tyr Lys Val Glu
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 Asp Leu Phe Ile Gly His Ile Ala Gly Met Asp Thr Phe Ala Leu Gly
 385 390 395 400
 Phe Lys Val Ala Tyr Lys Leu Val Lys Asp Gly Val Leu Asp Lys Phe
 405 410 415
 Ile Glu Glu Lys Tyr Arg Ser Phe Arg Glu Gly Ile Gly Arg Asp Ile
 420 425 430
 Val Glu Gly Lys Val Asp Phe Glu Lys Leu Glu Glu Tyr Ile Ile Asp
 435 440 445
 Lys Glu Thr Ile Glu Leu Pro Ser Gly Lys Gln Glu Tyr Leu Glu Ser
 450 455 460
 Leu Ile Asn Ser Tyr Ile Val Lys Thr Ile Leu Glu Leu Arg
 465 470 475

<210> 45

<211> 1095

<212> PRT

<213> Aspergillus shirousami

<400> 45

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 Ala Asp Gln Lys Tyr Cys Gly Gly Thr Trp Gln Gly Ile Ile Asp Lys
 35 40 45
 Leu Asp Tyr Ile Gln Gly Met Gly Phe Thr Ala Ile Trp Ile Thr Pro
 50 55 60
 Val Thr Ala Gln Leu Pro Gln Thr Thr Ala Tyr Gly Asp Ala Tyr His
 65 70 75 80
 Gly Tyr Trp Gln Gln Asp Ile Tyr Ser Leu Asn Glu Asn Tyr Gly Thr
 85 90 95
 Ala Asp Asp Leu Lys Ala Leu Ser Ser Ala Leu His Glu Arg Gly Met
 100 105 110
 Tyr Leu Met Val Asp Val Val Ala Asn His Met Gly Tyr Asp Gly Ala
 115 120 125
 Gly Ser Ser Val Asp Tyr Ser Val Phe Lys Pro Phe Ser Ser Gln Asp
 130 135 140
 Tyr Phe His Pro Phe Cys Phe Ile Gln Asn Tyr Glu Asp Gln Thr Gln
 145 150 155 160
 Val Glu Asp Cys Trp Leu Gly Asp Asn Thr Val Ser Leu Pro Asp Leu
 165 170 175
 Asp Thr Thr Lys Asp Val Val Lys Asn Glu Trp Tyr Asp Trp Val Gly
 180 185 190
 Ser Leu Val Ser Asn Tyr Ser Ile Asp Gly Leu Arg Ile Asp Thr Val
 195 200 205
 Lys His Val Gln Lys Asp Phe Trp Pro Gly Tyr Asn Lys Ala Ala Gly
 210 215 220
 Val Tyr Cys Ile Gly Glu Val Leu Asp Val Asp Pro Ala Tyr Thr Cys
 225 230 235 240
 Pro Tyr Gln Asn Val Met Asp Gly Val Leu Asn Tyr Pro Ile Tyr Tyr
 245 250 255
 Pro Leu Leu Asn Ala Phe Lys Ser Thr Ser Gly Ser Met Asp Asp Leu
 260 265 270
 Tyr Asn Met Ile Asn Thr Val Lys Ser Asp Cys Pro Asp Ser Thr Leu
 275 280 285
 Leu Gly Thr Phe Val Glu Asn His Asp Asn Pro Arg Phe Ala Ser Tyr
 290 295 300
 Thr Asn Asp Ile Ala Leu Ala Lys Asn Val Ala Ala Phe Ile Ile Leu
 305 310 315 320
 Asn Asp Gly Ile Pro Ile Ile Tyr Ala Gly Gln Glu Gln His Tyr Ala

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Pro	Thr	Asp	Ser	340	Glu	Leu	Tyr	Lys	Leu	345	Ile	Ala	Ser	Ala	Asn	350	Ala	Ile
Arg	Asn	Tyr	Ala	355	Ile	Ser	Lys	Asp	Thr	360	Gly	Phe	Val	Thr	Tyr	365	Lys	Asn
Trp	Pro	Ile	Tyr	370	Lys	Asp	Thr	Thr	Ile	375	Ala	Met	Arg	Lys	Gly	380	Thr	
385	Asp	Gly	Ser	Gln	390	Ile	Val	Thr	Ile	395	Leu	Ser	Asn	Lys	Gly	400	Ala	Ser
Asp	Ser	Tyr	Thr	405	Leu	Ser	Leu	Ser	Gly	410	Ala	Gly	Tyr	Thr	Ala	415	Gly	Gln
Gln	Leu	Thr	Glu	420	Val	Ile	Gly	Cys	Thr	425	Thr	Val	Thr	Val	Gly	430	Ser	Asp
Gly	Asn	Val	Pro	435	Val	Pro	Met	Ala	Gly	440	Gly	Leu	Pro	Arg	Val	445	Leu	Tyr
Pro	Thr	Glu	Lys	450	Leu	Ala	Gly	Ser	Lys	455	Ile	Cys	Ser	Ser	Ser	460	Lys	Pro
465	Ala	Thr	Leu	Asp	Ser	Trp	Leu	Ser	Asn	470	Glu	Ala	Thr	Val	Ala	475	Arg	Thr
Ala	Ile	Leu	Asn	485	Asn	Ile	Gly	Ala	Asp	490	Gly	Ala	Trp	Val	Ser	495	Gly	Ala
Asp	Ser	Gly	Ile	500	Val	Val	Ala	Ser	Pro	505	Ser	Thr	Asp	Asn	Pro	510	Asp	Tyr
Phe	Tyr	Thr	Trp	515	Thr	Arg	Asp	Ser	Gly	520	Ile	Val	Leu	Lys	Thr	525	Leu	Val
Asp	Leu	Phe	Arg	530	Asn	Gly	Asp	Thr	Asp	535	Leu	Leu	Ser	Thr	Ile	540	Glu	His
545	Tyr	Ile	Ser	Ser	550	Gln	Ala	Ile	Ile	555	Gln	Gly	Val	Ser	Asn	560	Ser	Gly
Asp	Leu	Ser	Ser	565	Gly	Gly	Leu	Gly	Glu	570	Pro	Lys	Phe	Asn	Val	575	Asp	Glu
Thr	Ala	Tyr	Ala	580	Gly	Ser	Trp	Gly	Arg	585	Pro	Gln	Arg	Asp	Gly	590	Pro	Ala
Leu	Arg	Ala	Thr	595	Ala	Met	Ile	Gly	Phe	600	Gly	Gln	Trp	Leu	Leu	605	Asp	Asn
Gly	Tyr	Thr	Ser	610	Ala	Ala	Thr	Glu	Ile	615	Val	Trp	Pro	Leu	Val	620	Arg	Asn
625	Asp	Leu	Ser	Tyr	630	Val	Ala	Gln	Tyr	635	Trp	Asn	Gln	Thr	Gly	640	Tyr	Asp
Trp	Glu	Glu	Val	645	Asn	Gly	Ser	Ser	Phe	650	Phe	Thr	Ile	Ala	Val	655	Gln	His
Arg	Ala	Leu	Val	660	Glu	Gly	Ser	Ala	Phe	665	Ala	Thr	Ala	Val	Gly	670	Ser	Ser
Cys	Ser	Trp	Cys	675	Asp	Ser	Gln	Ala	Pro	680	Gln	Ile	Leu	Cys	Tyr	685	Leu	Gln
Ser	Phe	Trp	Thr	690	Gly	Ser	Tyr	Ile	Leu	695	Ala	Asn	Phe	Asp	Ser	700	Ser	Arg
705	Ser	Gly	Lys	Asp	710	Thr	Leu	Leu	Gly	715	Ser	Ile	His	Thr	Phe	720	Asp	
Pro	Glu	Ala	Gly	725	Cys	Asp	Asp	Ser	Thr	730	Phe	Gln	Pro	Cys	Ser	735	Pro	Arg
Ala	Leu	Ala	Asn	740	His	Lys	Glu	Val	Val	745	Asp	Ser	Phe	Arg	Ser	750	Ile	Tyr
Thr	Leu	Asn	Asp	755	Gly	Leu	Ser	Asp	Ser	760	Glu	Ala	Val	Ala	Val	765	Gly	Arg
Tyr	Pro	Glu	Asp	770	Ser	Tyr	Tyr	Asn	Gly	775	Asn	Pro	Trp	Phe	Leu	780	Cys	Thr
785	Leu	Ala	Ala	Ala	790	Gln	Leu	Tyr	Asp	795	Ala	Leu	Tyr	Gln	Trp	800	Asp	Lys
Gln	Gly	Ser	Leu	805	Glu	Ile	Thr	Asp	Val	810	Ser	Leu	Asp	Phe	Phe	815	Lys	Ala
				820						825						830		

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Leu Tyr Ser Gly Ala Ala Thr Gly Thr Tyr Ser Ser Ser Ser Thr
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 Tyr Ser Ser Ile Val Ser Ala Val Lys Thr Phe Ala Asp Gly Phe Val
 850 855 860
 Ser Ile Val Glu Thr His Ala Ala Ser Asn Gly Ser Leu Ser Glu Gln
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 Phe Asp Lys Ser Asp Gly Asp Glu Leu Ser Ala Arg Asp Leu Thr Trp
 885 890 895
 Ser Tyr Ala Ala Leu Leu Thr Ala Asn Asn Arg Arg Asn Ser Val Val
 900 905 910
 Pro Pro Ser Trp Gly Glu Thr Ser Ala Ser Ser Val Pro Gly Thr Cys
 915 920 925
 Ala Ala Thr Ser Ala Ser Gly Thr Tyr Ser Ser Val Thr Val Thr Ser
 930 935 940
 Trp Pro Ser Ile Val Ala Thr Gly Gly Thr Thr Thr Ala Thr Thr
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 965 970 975
 Ser Lys Thr Ser Thr Thr Thr Ser Ser Thr Ser Cys Thr Thr Pro Thr
 980 985 990
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 995 1000 1005
 Asn Ile Tyr Leu Val Gly Ser Ile Ser Gln Leu Gly Asp Trp Glu Thr
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 Pro Trp Tyr Val Thr Val Thr Leu Pro Ala Gly Glu Ser Phe Glu Tyr
 1045 1050 1055
 Lys Phe Ile Arg Val Glu Ser Asp Asp Ser Val Glu Trp Glu Ser Asp
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<210> 46

<211> 3285

<212> DNA

<213> *Aspergillus shirousami*

<400> 46

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 tggatcacc cggtgaccgc ccagctcccc cagaccaccg cctacggcga cgcctaccac 240
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<210> 47

<211> 679

<212> PRT

<213> Thermoanaerobacterium thermosaccharolyticum

<400> 47

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35     40     45
Arg Val Trp Phe Thr Leu Ala Asn Gly Ala Ile Ser Glu Val Tyr Tyr
50     55     60
Pro Thr Ile Asp Thr Ala Asp Val Lys Glu Ile Lys Phe Ile Val Thr
65     70     75     80
Asp Gly Lys Ser Phe Val Ser Asp Glu Thr Lys Asp Ala Ile Ser Lys
85     90     95
Val Glu Lys Phe Thr Asp Lys Ser Leu Gly Tyr Lys Leu Val Asn Thr
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Lys Arg Asn Ser Leu Ile Met Lys Ala Lys Phe Glu Ala Leu Glu Gly
130    135    140
Ser Ile His Asp Tyr Lys Leu Tyr Leu Ala Tyr Asp Pro His Ile Lys
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165    170    175

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 210 215 220
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 225 230 235 240
 Asn Ser Glu Phe Glu Ile Val Leu Ser Phe Gly Gly Ser Asp Ser Glu
 245 250 255
 Ala Ala Lys Thr Ala Leu Glu Thr Leu Gly Glu Asp Tyr Asn Asn Leu
 260 265 270
 Lys Asn Asn Tyr Ile Asp Glu Trp Thr Lys Tyr Cys Asn Thr Leu Asn
 275 280 285
 Asn Phe Asn Gly Lys Ala Asn Ser Leu Tyr Tyr Asn Ser Met Met Ile
 290 295 300
 Leu Lys Ala Ser Glu Asp Lys Thr Asn Lys Gly Ala Tyr Ile Ala Ser
 305 310 315 320
 Leu Ser Ile Pro Trp Gly Asp Gly Gln Arg Asp Asp Asn Thr Gly Gly
 325 330 335
 Tyr His Leu Val Trp Ser Arg Asp Leu Tyr His Val Ala Asn Ala Phe
 340 345 350
 Ile Ala Ala Gly Asp Val Asp Ser Ala Asn Arg Ser Leu Asp Tyr Leu
 355 360 365
 Ala Lys Val Val Lys Asp Asn Gly Met Ile Pro Gln Asn Thr Trp Ile
 370 375 380
 Ser Gly Lys Pro Tyr Trp Thr Ser Ile Gln Leu Asp Glu Gln Ala Asp
 385 390 395 400
 Pro Ile Ile Leu Ser Tyr Arg Leu Lys Arg Tyr Asp Leu Tyr Asp Ser
 405 410 415
 Leu Val Lys Pro Leu Ala Asp Phe Ile Ile Lys Ile Gly Pro Lys Thr
 420 425 430
 Gly Gln Glu Arg Trp Glu Glu Ile Gly Gly Tyr Ser Pro Ala Thr Met
 435 440 445
 Ala Ala Glu Val Ala Gly Leu Thr Cys Ala Ala Tyr Ile Ala Glu Gln
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 Asn Lys Asp Tyr Glu Ser Ala Gln Lys Tyr Gln Glu Lys Ala Asp Asn
 465 470 475 480
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 Gly Asn Gly Gln Tyr Tyr Ile Arg Ile Ala Gly Leu Ser Asp Pro Asn
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 515 520 525
 Lys Glu Ile Val Asp Pro Ser Phe Leu Glu Leu Val Arg Leu Gly Val
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 Lys Ser Ala Asp Asp Pro Lys Ile Leu Asn Thr Leu Lys Val Val Asp
 545 550 555 560
 Ser Thr Ile Lys Val Asp Thr Pro Lys Gly Pro Ser Trp Tyr Arg Tyr
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 580 585 590
 Ala Gly Lys Gly Arg Leu Trp Pro Leu Leu Thr Gly Glu Arg Gly Met
 595 600 605
 Tyr Glu Ile Ala Ala Gly Lys Asp Ala Thr Pro Tyr Val Lys Ala Met
 610 615 620
 Glu Lys Phe Ala Asn Glu Gly Gly Ile Ile Ser Glu Gln Val Trp Glu
 625 630 635 640
 Asp Thr Gly Leu Pro Thr Asp Ser Ala Ser Pro Leu Asn Trp Ala His
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 Asp Met Pro Asp Ile Val Tyr

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 <211> 2037
 <212> DNA
 <213> Thermoanaerobacterium thermosaccharolyticum

<220>
 <223> synthetic

<400> 48
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 gaggtgtact acccgaccat cgacaccgcc gacgtgaagg agatcaagtt catcgtgacc 240
 gacggcaagt ccttcgtgtc cgacgagacc aaggacgcca tctccaaggt ggagaagttc 300
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 aaccagggct cctacaacga gggctacgtg atcaaggcca acaacaacga gatgctcatg 540
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<210> 49
 <211> 579
 <212> PRT
 <213> Rhizopus oryzae

<400> 49
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 35 40 45
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 Ser Asn Tyr Glu Tyr Trp Thr Phe Ser Ala Ser Ile Asn Gly Ile Lys
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Thr	Ala	Thr	Ala	Thr	Thr	Thr	Thr	Ala	Pro	Ser	Thr	Ser	Thr	Thr	Thr
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Leu	Arg	Asn	Ile	Asn	Pro	Pro	Gly	Ser	Ala	Thr	Gly	Phe	Ile	Ala	Ala
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Ser	Leu	Ser	Thr	Ala	Gly	Pro	Asp	Tyr	Tyr	Tyr	Ala	Trp	Thr	Arg	Asp
			180					185					190		
Ala	Ala	Leu	Thr	Ser	Asn	Val	Ile	Val	Tyr	Glu	Tyr	Asn	Thr	Thr	Leu
			195					200				205			
Ser	Gly	Asn	Lys	Thr	Ile	Leu	Asn	Val	Leu	Lys	Asp	Tyr	Val	Thr	Phe
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225					230					235					240
Pro	Lys	Phe	Asn	Pro	Asp	Ala	Ser	Gly	Tyr	Thr	Gly	Ala	Trp	Gly	Arg
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Ala	Asp	Ser	Tyr	Leu	Thr	Gln	Thr	Lys	Asp	Ala	Ser	Tyr	Val	Thr	Gly
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Thr	Leu	Lys	Pro	Ala	Ile	Phe	Lys	Asp	Leu	Asp	Tyr	Val	Val	Asn	Val
					295						300				
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305					310					315					320
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				325					330					335	
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Val	Ala	Val	Glu	Asp	Ser	Phe	Ala	Ser	Leu	Tyr	Pro	Ile	Asn	Lys	Asn
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465					470					475					480
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Leu	Ser	Thr	Val	Gln	Leu	His	Ala	His	Asn	Asn	Gly	Ser	Leu	Ala	Glu
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Trp	Ser	His	Ala	Ser	Leu	Ile	Thr	Ala	Ser	Tyr	Ala	Lys	Ala	Gly	Ala
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60110USPCT1 Corrected SEQ LIST 2-2007.txt

<210> 50
 <211> 1737
 <212> DNA
 <213> *Rhizopus oryzae*

<400> 50
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 tccctcgccg aggagttcga ccgcaccacc ggcctctcca ccggcgcccc cgacctacc 1680
 tggctccacg cctccctcat caccgcctcc tacgccaagg ccggcgcccc ggccgcc 1737

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 <211> 439
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 51
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 Gln Gly Phe Asn Trp Glu Ser Trp Lys Lys Gln Gly Gly Trp Tyr Asn
 35 40 45
 Tyr Leu Leu Gly Arg Val Asp Asp Ile Ala Ala Thr Gly Ala Thr His
 50 55 60
 Val Trp Leu Pro Gln Pro Ser His Ser Val Ala Pro Gln Gly Tyr Met
 65 70 75 80
 Pro Gly Arg Leu Tyr Asp Leu Asp Ala Ser Lys Tyr Gly Thr His Ala
 85 90 95
 Glu Leu Lys Ser Leu Thr Ala Ala Phe His Ala Lys Gly Val Gln Cys
 100 105 110
 Val Ala Asp Val Val Ile Asn His Arg Cys Ala Asp Tyr Lys Asp Gly
 115 120 125

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Arg Gly Ile Tyr Cys Val Phe Glu Gly Gly Thr Pro Asp Ser Arg Leu
 130 135 140
 Asp Trp Gly Pro Asp Met Ile Cys Ser Asp Asp Thr Gln Tyr Ser Asn
 145 150 155 160
 Gly Arg Gly His Arg Asp Thr Gly Ala Asp Phe Ala Ala Ala Pro Asp
 165 170 175
 Ile Asp His Leu Asn Pro Arg Val Gln Gln Glu Leu Ser Asp Trp Leu
 180 185 190
 Asn Trp Leu Lys Ser Asp Leu Gly Phe Asp Gly Trp Arg Leu Asp Phe
 195 200 205
 Ala Lys Gly Tyr Ser Ala Ala Val Ala Lys Val Tyr Val Asp Ser Thr
 210 215 220
 Ala Pro Thr Phe Val Val Ala Glu Ile Trp Ser Ser Leu His Tyr Asp
 225 230 235 240
 Gly Asn Gly Glu Pro Ser Ser Asn Gln Asp Ala Asp Arg Gln Glu Leu
 245 250 255
 Val Asn Trp Ala Gln Ala Val Gly Gly Pro Ala Ala Ala Phe Asp Phe
 260 265 270
 Thr Thr Lys Gly Val Leu Gln Ala Ala Val Gln Gly Glu Leu Trp Arg
 275 280 285
 Met Lys Asp Gly Asn Gly Lys Ala Pro Gly Met Ile Gly Trp Leu Pro
 290 295 300
 Glu Lys Ala Val Thr Phe Val Asp Asn His Asp Thr Gly Ser Thr Gln
 305 310 315 320
 Asn Ser Trp Pro Phe Pro Ser Asp Lys Val Met Gln Gly Tyr Ala Tyr
 325 330 335
 Ile Leu Thr His Pro Gly Thr Pro Cys Ile Phe Tyr Asp His Val Phe
 340 345 350
 Asp Trp Asn Leu Lys Gln Glu Ile Ser Ala Leu Ser Ala Val Arg Ser
 355 360 365
 Arg Asn Gly Ile His Pro Gly Ser Glu Leu Asn Ile Leu Ala Ala Asp
 370 375 380
 Gly Asp Leu Tyr Val Ala Lys Ile Asp Asp Lys Val Ile Val Lys Ile
 385 390 395 400
 Gly Ser Arg Tyr Asp Val Gly Asn Leu Ile Pro Ser Asp Phe His Ala
 405 410 415
 Val Ala His Gly Asn Asn Tyr Cys Val Trp Glu Lys His Gly Leu Arg
 420 425 430
 Val Pro Ala Gly Arg His His
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<210> 52

<211> 1320

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 52

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 ttgggctccc agctggccca atcccagggtc ctcttcagg ggttcaactg ggagtcgtgg 120
 aagaagcaag gtgggtggtg caactacctc ctggggcggg tggacgacat cgccgcgacg 180
 ggggccacgc acgtctggct cccgcagccg tcgcactcgg tggcgccgca ggggtacatg 240
 cccggccggc tctacgacct ggacgcgtcc aagtacggca cccacgcgga gctcaagtgc 300
 ctacaccgcg cgttccacgc caagggcgtc cagtgcgtcg ccgacgtcgt gatcaaccac 360
 cgctgcgccg actacaagga cggccgcggc atctactcgc tcttcgaggg cggcacgccc 420
 gacagccgcc tcgactgggg ccccgacatg atctgcagcg acgacacgca gtactccaac 480
 gggcgcgggc accgcgacac gggggccgac ttcgccgccc cgcccacat cgaccacctc 540
 aaccgcgctg tgcagcagga gctctcggac tggctcaact ggctcaagtc cgacctcggc 600
 ttgcacggct ggcgcctcga cttcgccaag ggctactccg ccgcccgtcg caaggtgtac 660
 gtcgacagca ccgccccac cttcgtcgtc gccgagatat ggagctccct ccactacgac 720

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ggcaacggcg agccgtccag caaccaggac gccgacaggc aggagctggt caactgggcg 780
caggcggtgg gcggcccccgc cgcggcggtc gacttcacca ccaagggcgt gctgcaggcg 840
gccgtccagg gcgagctgtg gcgcatgaag gacggcaacg gcaaggcgcc cgggatgac 900
ggctggctgc cggagaaggc cgtcacgttc gtcgacaacc acgacaccgg ctccacgcag 960
aactcgtggc cattcccttc cgacaaggct atgcagggct acgcctatat cctcacgcac 1020
ccaggaactc catgcatctt ctacgaccac gttttcgact ggaacctgaa gcaggagatc 1080
agcgcgctgt ctgcggtgag gtcaagaaac gggatccacc cggggagcga gctgaacatc 1140
ctcgccgccg acggggatct ctacgtcgcc aagattgacg acaaggatcat cgtgaagatc 1200
gggtcacggg acgacgtcgg gaacctgata ccctcagact tccacgccgt tgcccctggc 1260
aacaactact gcgtttggga gaagcacggg ctgagagttc cagcggggcg gcaccactag 1320

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<210> 53
 <211> 45
 <212> PRT
 <213> Artificial sequence

<220>
 <223> synthetic

<400> 53
 Ala Thr Gly Gly Thr Thr Thr Thr Ala Thr Thr Thr Gly Ser Gly Gly
 1 5 10 15
 Val Thr Ser Thr Ser Lys Thr Thr Thr Thr Ala Ser Lys Thr Ser Thr
 20 25 30
 Thr Thr Ser Ser Thr Ser Cys Thr Thr Pro Thr Ala Val
 35 40 45

<210> 54
 <211> 137
 <212> DNA
 <213> Artificial sequence
 <220>
 <223> synthetic

<400> 54
 gccaccggcg gcaccaccac caccgccacc accaccggct ccggcggcgt gacctccacc 60
 tccaagacca ccaccaccgc ctccaagacc tccaccacca cctcctccac ctccctgcacc 120
 accccgaccg ccgtgtc 137

<210> 55
 <211> 300
 <212> PRT
 <213> Pyrococcus furiosus

<400> 55
 Ile Tyr Phe Val Glu Lys Tyr His Thr Ser Glu Asp Lys Ser Thr Ser
 1 5 10 15
 Asn Thr Ser Ser Thr Pro Pro Gln Thr Thr Leu Ser Thr Thr Lys Val
 20 25 30
 Leu Lys Ile Arg Tyr Pro Asp Asp Gly Glu Trp Pro Gly Ala Pro Ile
 35 40 45
 Asp Lys Asp Gly Asp Gly Asn Pro Glu Phe Tyr Ile Glu Ile Asn Leu
 50 55 60
 Trp Asn Ile Leu Asn Ala Thr Gly Phe Ala Glu Met Thr Tyr Asn Leu
 65 70 75 80
 Thr Ser Gly Val Leu His Tyr Val Gln Gln Leu Asp Asn Ile Val Leu
 85 90 95
 Arg Asp Arg Ser Asn Trp Val His Gly Tyr Pro Glu Ile Phe Tyr Gly
 100 105 110
 Asn Lys Pro Trp Asn Ala Asn Tyr Ala Thr Asp Gly Pro Ile Pro Leu
 115 120 125

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Pro Ser Lys Val Ser Asn Leu Thr Asp Phe Tyr Leu Thr Ile Ser Tyr
 130 135 140
 Lys Leu Glu Pro Lys Asn Gly Leu Pro Ile Asn Phe Ala Ile Glu Ser
 145 150 155 160
 Trp Leu Thr Arg Glu Ala Trp Arg Thr Thr Gly Ile Asn Ser Asp Glu
 165 170 175
 Gln Glu Val Met Ile Trp Ile Tyr Tyr Asp Gly Leu Gln Pro Ala Gly
 180 185 190
 Ser Lys Val Lys Glu Ile Val Val Pro Ile Ile Val Asn Gly Thr Pro
 195 200 205
 Val Asn Ala Thr Phe Glu Val Trp Lys Ala Asn Ile Gly Trp Glu Tyr
 210 215 220
 Val Ala Phe Arg Ile Lys Thr Pro Ile Lys Glu Gly Thr Val Thr Ile
 225 230 235 240
 Pro Tyr Gly Ala Phe Ile Ser Val Ala Ala Asn Ile Ser Ser Leu Pro
 245 250 255
 Asn Tyr Thr Glu Leu Tyr Leu Glu Asp Val Glu Ile Gly Thr Glu Phe
 260 265 270
 Gly Thr Pro Ser Thr Thr Ser Ala His Leu Glu Trp Trp Ile Thr Asn
 275 280 285
 Ile Thr Leu Thr Pro Leu Asp Arg Pro Leu Ile Ser
 290 295 300

<210> 56
 <211> 903
 <212> DNA
 <213> Pyrococcus furiosus

<400> 56
 atctacttcg tggagaagta ccacacctcc gaggacaagt ccacctccaa cacctcctcc 60
 accccgccgc agaccaccct ctccaccacc aagggtgctca agatccgcta cccggacgac 120
 ggcgagtggc ccggcgcccc gatcgacaag gacggcgacg gcaacccgga gttctacatc 180
 gagatcaacc tctggaacat cctcaacgcc accggcttcg ccgagatgac ctacaacctc 240
 actagtggcg tgctccacta cgtgcagcag ctcgacaaca tcgtgctccg cgaccgctcc 300
 aactgggtgc acggctaccc ggaaatcttc tacggcaaca agccgtggaa cgccaactac 360
 gccaccgacg gcccgatccc gctcccgtcc aagggtgtcca acctcaccga cttctacctc 420
 accatctctt acaagctcga gccgaagaac ggctctccga tcaacttcgc catcgagtcc 480
 tggctcaccg gcgaggcctg gcgcaccacc ggcatacaact ccgacgagca ggaggtgatg 540
 atctggatct actacgacgg cctccagccc gcgggctcca aggtgaagga gatcgtgggtg 600
 ccgatcatcg tgaacggcac cccggtgaac gccaccttcg aggtgtggaa ggccaacatc 660
 ggctgggagt acgtggcctt ccgcatcaag accccgatca aggagggcac cgtgaccatc 720
 ccgtacggcg ccttcatctc cgtggccgcc aacatctcct ccctcccgaa ctacaccgag 780
 aagtacctcg aggacgtgga gatcggcacc gagttcggca ccccgccac cacctccgac 840
 cacctcgagt ggtggatcac caacatcacc ctcaccccg ctcgaccgcc gctcatctcc 900
 tag 903

<210> 57
 <211> 387
 <212> PRT
 <213> Thermus flavus

<400> 57
 Met Tyr Glu Pro Lys Pro Glu His Arg Phe Thr Phe Gly Leu Trp Thr
 1 5 10 15
 Val Asp Asn Val Asp Arg Asp Pro Phe Gly Asp Thr Val Arg Glu Arg
 20 25 30
 Leu Asp Pro Val Tyr Val Val His Lys Leu Ala Glu Leu Gly Ala Tyr
 35 40 45
 Gly Val Asn Leu His Asp Glu Asp Leu Ile Pro Arg Gly Thr Pro Pro
 50 55 60
 Gln Glu Arg Asp Gln Ile Val Arg Arg Phe Lys Lys Ala Leu Asp Glu
 65 70 75 80

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Thr Val Leu Lys Val Pro Met Val Thr Ala Asn Leu Phe Ser Glu Pro
 85 90 95
 Ala Phe Arg Asp Gly Ala Ser Thr Thr Arg Asp Pro Trp Val Trp Ala
 100 105 110
 Tyr Ala Leu Arg Lys Ser Leu Glu Thr Met Asp Leu Gly Ala Glu Leu
 115 120 125
 Gly Ala Glu Ile Tyr Met Phe Trp Met Val Arg Glu Arg Ser Glu Val
 130 135 140
 Glu Ser Thr Asp Lys Thr Arg Lys Val Trp Asp Trp Val Arg Glu Thr
 145 150 155 160
 Leu Asn Phe Met Thr Ala Tyr Thr Glu Asp Gln Gly Tyr Gly Tyr Arg
 165 170 175
 Phe Ser Val Glu Pro Lys Pro Asn Glu Pro Arg Gly Asp Ile Tyr Phe
 180 185 190
 Thr Thr Val Gly Ser Met Leu Ala Leu Ile His Thr Leu Asp Arg Pro
 195 200 205
 Glu Arg Phe Gly Leu Asn Pro Glu Phe Ala His Glu Thr Met Ala Gly
 210 215 220
 Leu Asn Phe Asp His Ala Val Ala Gln Ala Val Asp Ala Gly Lys Leu
 225 230 235 240
 Phe His Ile Asp Leu Asn Asp Gln Arg Met Ser Arg Phe Asp Gln Asp
 245 250 255
 Leu Arg Phe Gly Ser Glu Asn Leu Lys Ala Gly Phe Phe Leu Val Asp
 260 265 270
 Leu Leu Glu Ser Ser Gly Tyr Gln Gly Pro Arg His Phe Glu Ala His
 275 280 285
 Ala Leu Arg Thr Glu Asp Glu Glu Gly Val Trp Thr Phe Val Arg Val
 290 295 300
 Cys Met Arg Thr Tyr Leu Ile Ile Lys Val Arg Ala Glu Thr Phe Arg
 305 310 315 320
 Glu Asp Pro Glu Val Lys Glu Leu Leu Ala Ala Tyr Tyr Gln Glu Asp
 325 330 335
 Pro Ala Thr Leu Ala Leu Leu Asp Pro Tyr Ser Arg Glu Lys Ala Glu
 340 345 350
 Ala Leu Lys Arg Ala Glu Leu Pro Leu Glu Thr Lys Arg Arg Arg Gly
 355 360 365
 Tyr Ala Leu Glu Arg Leu Asp Gln Leu Ala Val Glu Tyr Leu Leu Gly
 370 375 380
 Val Arg Gly
 385

<210> 58
 <211> 978
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 58
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 gcgtccggcc atcaaatacta ctctgtggag aagtaccaca cctccgaggga caagtccacc 120
 tccaacacct cctccacccc gccgcagacc accctctcca ccaccaaggt gctcaagatc 180
 cgctaccggg acgacgggtga gtggcccgcc gccccgatcg acaaggacgg cgacggcaac 240
 ccggagttct acatcgagat caacctctgg aacatcctca acgccaccgg ctctgccgag 300
 atgacctaca acctcactag tggcgtgctc cactacgtgc agcagctcga caacatcgtg 360
 ctccgcgacc gctccaactg ggtgcacggc tacccggaaa tcttctacgg caacaagccg 420
 tggaaacgcca actacgccac cgacggcccc atcccgtctc cgtccaaggt gtccaacctc 480
 accgacttct acctcaccat ctctacaag ctcgagccga agaacggtct cccgatcaac 540
 ttcgccatcg agtcctggct caccgcgag gcctggcgca ccaccggcat caactccgac 600
 gagcaggagg tgatgatctg gatctactac gacggcctcc agcccgcggg ctccaagggtg 660
 aaggagatcg tgggtccgat catcgtgaac ggcaccccgg tgaacgccac ctctgagggtg 720

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tggaaggcca	acatcggtcg	ggagtagctg	gccttccgca	tcaagacccc	gatcaaggag	780
ggcaccgtga	ccatcccgtg	cggcgccttc	atctccgtgg	ccgccaacat	ctcctccctc	840
ccgaactaca	ccgagaagta	cctcgaggac	gtggagatcg	gcaccgagtt	cggcaccccg	900
tccaccacct	ccgcccacct	cgagtgggtg	atcaccaaca	tcaccctcac	cccgtctcgac	960
cgcccgctca	tctcctag					978

<210> 59

<211> 1920

<212> DNA

<213> *Aspergillus niger*

<400> 59

atgtccttcc	gctccctcct	cgccctctcc	ggcctcgtgt	gcaccggcct	cgccaacgtg	60
atctccaagc	gcgccaccct	cgactcctgg	ctctccaacg	aggccaccgt	ggcccgacc	120
gccatcctca	acaacatcgg	cgccgacggc	gcctgggtgt	ccggcgccga	ctccggcatc	180
gtgggtggcct	ccccgtccac	cgacaacccg	gactacttct	acacctggac	ccgcgactcc	240
ggcctcgtgc	tcaagaccct	cgtggacctc	ttccgcaacg	gcgacacctc	cctcctctcc	300
accatcgaga	actacatctc	cgcccaggcc	atcgtgcagg	gcatctccaa	cccgtccggc	360
gacctctcct	ccggcgccgg	cctcggcgag	ccgaagtcca	acgtggacga	gaccgcctac	420
accggtctct	ggggcgcccc	gcagcgcgac	ggcccgcccc	tccgcgccac	cgccatgatc	480
ggcttcggcc	agtggctcct	cgacaacggc	tacacctcca	ccgccaccga	catcgtgtgg	540
ccgctcgtgc	gcaacgacct	ctcctacgtg	gcccagttact	ggaaccagac	cggtctacgac	600
ctctgggagg	aggtgaacgg	ctcctccttc	ttcaccatcg	ccgtgcagca	ccgcgccctc	660
gtggagggct	ccgccttcgc	caccgcccgtg	ggctcctcct	gctcctgggtg	cgactcccag	720
gccccggaga	tcctctgcta	cctccagttc	ttctggaccg	gctccttcat	cctcgccaac	780
ttcgactcct	cccgtctcgg	caaggacgcc	aacaccctcc	tcggctccat	ccacaccttc	840
gacccgagg	ccgcctgcga	cgactccacc	ttccagccgt	gctccccgcy	cgccctcgcc	900
aaccacaagg	aggtgggtgga	ctccttccgc	tccatctaca	ccctcaacga	cggcctctcc	960
gactccgagg	ccgtggccgt	gggcccgtac	ccggaggaca	cctactacaa	cggaaccccg	1020
tggttcctct	gcaccctcgc	cgccgcccag	cagctctacg	acgcccctta	ccagtgggac	1080
aagcagggct	ccctcgaggt	gaccgacgtg	tcctctgact	tcttcaaggc	cctctactcc	1140
gacgcccga	ccggcaccta	ctcctcctcc	tcctccacct	actcctccat	cgtaggacgc	1200
gtgaagacct	tcgcccagcg	cttcgtgtcc	atcgtggaga	cccacgcccgc	ctccaacggc	1260
tccatgtccg	agcagtacga	caagtccgac	ggcgagcagc	tctccgccccg	cgacctcacc	1320
tggctctacg	ccgcccctct	caccgccaac	aaccgcccga	actccgtgggt	gccggcctcc	1380
tggggcgaga	cctccgcttc	ctccgtgccc	ggcacctgcy	ccgccacctc	cgccatcggc	1440
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accaccgcca	ccccgaccgg	ctccggctcc	gtgacctcca	cctccaagac	caccgccacc	1560
gcctccaaga	cctccacctc	cacctcctcc	acctcctgca	ccaccccgc	cgccgtggcc	1620
gtgaccttcg	acctcaccgc	caccaccacc	tacggcgaga	acatctacct	cgtagggctcc	1680
atctcccagc	tcggcgactg	ggagacctcc	gacggcatcg	ccctctccgc	cgacaagtac	1740
acctcctccg	acccgctctg	gtacgtgacc	gtgaccttcc	cggccggcga	gtccttcgag	1800
tacaagttca	tccgcatacga	gtccgacgac	tccgtggagt	gggagtccga	cccgaaccgc	1860
gagtacaccg	tgccgcaggc	ctgcggcacc	tccaccgcca	ccgtgaccga	cacctggcgc	1920

<210> 60

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 60

Ser Glu Lys Asp Glu Leu

1

5

<210> 61

<211> 561

<212> DNA

<213> Artificial Sequence

<220>

<223> xylanase BD7436

<220>

<221> CDS

<222> (1)..(561)

<400> 61

atg	gct	agc	acc	ttc	tac	tgg	cat	ttg	tgg	acc	gac	ggc	atc	ggc	acc	48
Met	Ala	Ser	Thr	Phe	Tyr	Trp	His	Leu	Trp	Thr	Asp	Gly	Ile	Gly	Thr	
1				5				10					15			

gtg	aac	gct	acc	aac	ggc	agc	gac	ggc	aac	tac	agc	gtg	agc	tgg	agc	96
Val	Asn	Ala	Thr	Asn	Gly	Ser	Asp	Gly	Asn	Tyr	Ser	Val	Ser	Trp	Ser	
			20					25					30			

aac	tgc	ggc	aac	ttc	gtg	gtg	ggc	aag	ggc	tgg	acc	acc	ggc	agc	gct	144
Asn	Cys	Gly	Asn	Phe	Val	Val	Gly	Lys	Gly	Trp	Thr	Thr	Gly	Ser	Ala	
		35					40					45				

acc	agg	gtg	atc	aac	tac	aac	gct	cat	gct	ttc	agc	gtg	gtg	ggc	aac	192
Thr	Arg	Val	Ile	Asn	Tyr	Asn	Ala	His	Ala	Phe	Ser	Val	Val	Gly	Asn	
		50				55					60					

gct	tac	ttg	gct	ttg	tac	ggc	tgg	acc	agg	aac	agc	ttg	atc	gag	tac	240
Ala	Tyr	Leu	Ala	Leu	Tyr	Gly	Trp	Thr	Arg	Asn	Ser	Leu	Ile	Glu	Tyr	
65					70					75				80		

tac	gtg	gtg	gac	agc	tgg	ggc	acc	tac	agg	cca	acc	ggc	acc	tac	aag	288
Tyr	Val	Val	Asp	Ser	Trp	Gly	Thr	Tyr	Arg	Pro	Thr	Gly	Thr	Tyr	Lys	
				85					90					95		

ggc	acc	gtg	acc	agc	gac	ggc	ggc	acc	tac	gac	atc	tac	acc	acc	acc	336
Gly	Thr	Val	Thr	Ser	Asp	Gly	Gly	Thr	Tyr	Asp	Ile	Tyr	Thr	Thr	Thr	
			100					105					110			

agg	acc	aac	gct	cca	agc	atc	gac	ggc	aac	aac	acc	acc	ttc	acc	caa	384
Arg	Thr	Asn	Ala	Pro	Ser	Ile	Asp	Gly	Asn	Asn	Thr	Thr	Phe	Thr	Gln	
		115					120					125				

ttc	tgg	agc	gtg	agg	caa	agc	aag	agg	cca	atc	ggc	acc	aac	aac	acc	432
Phe	Trp	Ser	Val	Arg	Gln	Ser	Lys	Arg	Pro	Ile	Gly	Thr	Asn	Asn	Thr	
	130					135					140					

atc	acc	ttc	agc	aac	cat	gtg	aac	gct	tgg	aag	agc	aag	ggc	atg	aac	480
Ile	Thr	Phe	Ser	Asn	His	Val	Asn	Ala	Trp	Lys	Ser	Lys	Gly	Met	Asn	
					150					155					160	

ttg	ggc	agc	agc	tgg	agc	tac	caa	gtg	ttg	gct	acc	gag	ggc	tac	caa	528
Leu	Gly	Ser	Ser	Trp	Ser	Tyr	Gln	Val	Leu	Ala	Thr	Glu	Gly	Tyr	Gln	
				165					170					175		

agc	agc	ggc	tac	agc	aac	gtg	acc	gtg	tgg	tag						561
Ser	Ser	Gly	Tyr	Ser	Asn	Val	Thr	Val	Trp							
			180					185								

<210> 62

<211> 186

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 62

Met Ala Ser Thr Phe Tyr Trp His Leu Trp Thr Asp Gly Ile Gly Thr
1 5 10 15

Val Asn Ala Thr Asn Gly Ser Asp Gly Asn Tyr Ser Val Ser Trp Ser
20 25 30

Asn Cys Gly Asn Phe Val Val Gly Lys Gly Trp Thr Thr Gly Ser Ala
35 40 45

Thr Arg Val Ile Asn Tyr Asn Ala His Ala Phe Ser Val Val Gly Asn
50 55 60

Ala Tyr Leu Ala Leu Tyr Gly Trp Thr Arg Asn Ser Leu Ile Glu Tyr
65 70 75 80

Tyr Val Val Asp Ser Trp Gly Thr Tyr Arg Pro Thr Gly Thr Tyr Lys
85 90 95

Gly Thr Val Thr Ser Asp Gly Gly Thr Tyr Asp Ile Tyr Thr Thr Thr
100 105 110

Arg Thr Asn Ala Pro Ser Ile Asp Gly Asn Asn Thr Thr Phe Thr Gln
115 120 125

Phe Trp Ser Val Arg Gln Ser Lys Arg Pro Ile Gly Thr Asn Asn Thr
130 135 140

Ile Thr Phe Ser Asn His Val Asn Ala Trp Lys Ser Lys Gly Met Asn
145 150 155 160

Leu Gly Ser Ser Trp Ser Tyr Gln Val Leu Ala Thr Glu Gly Tyr Gln
165 170 175

Ser Ser Gly Tyr Ser Asn Val Thr Val Trp
180 185

<210> 63

<211> 561

<212> DNA

<213> Artificial Sequence

<220>

<223> Xylanase BD6002A

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<220>

<221> CDS

<222> (1)..(561)

<400> 63

atg	gct	agc	acc	gac	tac	tgg	caa	aac	tgg	acc	gac	ggc	ggc	ggc	acc	48
Met	Ala	Ser	Thr	Asp	Tyr	Trp	Gln	Asn	Trp	Thr	Asp	Gly	Gly	Gly	Thr	
1				5					10					15		

gtg	aac	gct	acc	aac	ggc	agc	gac	ggc	aac	tac	agc	gtg	agc	tgg	agc	96
Val	Asn	Ala	Thr	Asn	Gly	Ser	Asp	Gly	Asn	Tyr	Ser	Val	Ser	Trp	Ser	
			20					25					30			

aac	tgc	ggc	aac	ttc	gtg	gtg	ggc	aag	ggc	tgg	acc	acc	ggc	agc	gct	144
Asn	Cys	Gly	Asn	Phe	Val	Val	Gly	Lys	Gly	Trp	Thr	Thr	Gly	Ser	Ala	
		35					40					45				

acc	agg	gtg	atc	aac	tac	aac	gct	ggc	gct	ttc	agc	cca	agc	ggc	aac	192
Thr	Arg	Val	Ile	Asn	Tyr	Asn	Ala	Gly	Ala	Phe	Ser	Pro	Ser	Gly	Asn	
	50					55					60					

ggc	tac	ttg	gct	ttg	tac	ggc	tgg	acc	agg	aac	agc	ttg	atc	gag	tac	240
Gly	Tyr	Leu	Ala	Leu	Tyr	Gly	Trp	Thr	Arg	Asn	Ser	Leu	Ile	Glu	Tyr	
65				70					75					80		

tac	gtg	gtg	gac	agc	tgg	ggc	acc	tac	agg	cca	acc	ggc	acc	tac	aag	288
Tyr	Val	Val	Asp	Ser	Trp	Gly	Thr	Tyr	Arg	Pro	Thr	Gly	Thr	Tyr	Lys	
			85						90					95		

ggc	acc	gtg	acc	agc	gac	ggc	ggc	acc	tac	gac	atc	tac	acc	acc	acc	336
Gly	Thr	Val	Thr	Ser	Asp	Gly	Gly	Thr	Tyr	Asp	Ile	Tyr	Thr	Thr	Thr	
			100					105					110			

agg	acc	aac	gct	cca	agc	atc	gac	ggc	aac	aac	acc	acc	ttc	acc	caa	384
Arg	Thr	Asn	Ala	Pro	Ser	Ile	Asp	Gly	Asn	Asn	Thr	Thr	Phe	Thr	Gln	
		115					120					125				

ttc	tgg	agc	gtg	agg	caa	agc	aag	agg	cca	atc	ggc	acc	aac	aac	acc	432
Phe	Trp	Ser	Val	Arg	Gln	Ser	Lys	Arg	Pro	Ile	Gly	Thr	Asn	Asn	Thr	
	130					135					140					

atc	acc	ttc	agc	aac	cat	gtg	aac	gct	tgg	aag	agc	aag	ggc	atg	aac	480
Ile	Thr	Phe	Ser	Asn	His	Val	Asn	Ala	Trp	Lys	Ser	Lys	Gly	Met	Asn	
	145				150					155				160		

ttg	ggc	agc	agc	tgg	agc	tac	caa	gtg	ttg	gct	acc	gag	ggc	tac	caa	528
Leu	Gly	Ser	Ser	Trp	Ser	Tyr	Gln	Val	Leu	Ala	Thr	Glu	Gly	Tyr	Gln	
				165					170					175		

agc	agc	ggc	tac	agc	aac	gtg	acc	gtg	tgg	tag						561
Ser	Ser	Gly	Tyr	Ser	Asn	Val	Thr	Val	Trp							
			180					185								

<210> 64

<211> 186

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 64

Met Ala Ser Thr Asp Tyr Trp Gln Asn Trp Thr Asp Gly Gly Gly Thr
 1 5 10 15

Val Asn Ala Thr Asn Gly Ser Asp Gly Asn Tyr Ser Val Ser Trp Ser
 20 25 30

Asn Cys Gly Asn Phe Val Val Gly Lys Gly Trp Thr Thr Gly Ser Ala
 35 40 45

Thr Arg Val Ile Asn Tyr Asn Ala Gly Ala Phe Ser Pro Ser Gly Asn
 50 55 60

Gly Tyr Leu Ala Leu Tyr Gly Trp Thr Arg Asn Ser Leu Ile Glu Tyr
 65 70 75 80

Tyr Val Val Asp Ser Trp Gly Thr Tyr Arg Pro Thr Gly Thr Tyr Lys
 85 90 95

Gly Thr Val Thr Ser Asp Gly Gly Thr Tyr Asp Ile Tyr Thr Thr Thr
 100 105 110

Arg Thr Asn Ala Pro Ser Ile Asp Gly Asn Asn Thr Thr Phe Thr Gln
 115 120 125

Phe Trp Ser Val Arg Gln Ser Lys Arg Pro Ile Gly Thr Asn Asn Thr
 130 135 140

Ile Thr Phe Ser Asn His Val Asn Ala Trp Lys Ser Lys Gly Met Asn
 145 150 155 160

Leu Gly Ser Ser Trp Ser Tyr Gln Val Leu Ala Thr Glu Gly Tyr Gln
 165 170 175

Ser Ser Gly Tyr Ser Asn Val Thr Val Trp
 180 185

<210> 65

<211> 561

<212> DNA

<213> Artificial Sequence

<220>

<223> xylanase BD6002B

<220>

<221> CDS

<222> (1)..(561)

60110USPCT1 Corrected SEQ LIST 2-2007.txt

<400> 65
 atg gcc tcc acc gac tac tgg cag aac tgg acc gac ggc ggc ggc acc 48
 Met Ala Ser Thr Asp Tyr Trp Gln Asn Trp Thr Asp Gly Gly Gly Thr
 1 5 10 15

 gtg aac gcc acc aac ggc tcc gac ggc aac tac tcc gtg tcc tgg tcc 96
 Val Asn Ala Thr Asn Gly Ser Asp Gly Asn Tyr Ser Val Ser Trp Ser
 20 25 30

 aac tgc ggc aac ttc gtg gtg ggc aag ggc tgg acc acc ggc tcc gcc 144
 Asn Cys Gly Asn Phe Val Val Gly Lys Gly Trp Thr Thr Gly Ser Ala
 35 40 45

 acc cgc gtg atc aac tac aac gcc ggc gcc ttc tcc ccg tcc ggc aac 192
 Thr Arg Val Ile Asn Tyr Asn Ala Gly Ala Phe Ser Pro Ser Gly Asn
 50 55 60

 ggc tac ctc gcc ctc tac ggc tgg acc cgc aac tcc ctc atc gag tac 240
 Gly Tyr Leu Ala Leu Tyr Gly Trp Thr Arg Asn Ser Leu Ile Glu Tyr
 65 70 75 80

 tac gtg gtg gac tcc tgg ggc acc tac cgc ccg acc ggc acc tac aag 288
 Tyr Val Val Asp Ser Trp Gly Thr Tyr Arg Pro Thr Gly Thr Tyr Lys
 85 90 95

 ggc acc gtg acc tcc gac ggc ggc acc tac gac atc tac acc acc acc 336
 Gly Thr Val Thr Ser Asp Gly Gly Thr Tyr Asp Ile Tyr Thr Thr Thr
 100 105 110

 cgc acc aac gcc ccg tcc atc gac ggc aac aac acc acc ttc acc cag 384
 Arg Thr Asn Ala Pro Ser Ile Asp Gly Asn Asn Thr Thr Phe Thr Gln
 115 120 125

 ttc tgg tcc gtg cgc cag tcc aag cgc ccg atc ggc acc aac aac acc 432
 Phe Trp Ser Val Arg Gln Ser Lys Arg Pro Ile Gly Thr Asn Asn Thr
 130 135 140

 atc acc ttc tcc aac cac gtg aac gcc tgg aag tcc aag ggc atg aac 480
 Ile Thr Phe Ser Asn His Val Asn Ala Trp Lys Ser Lys Gly Met Asn
 145 150 155 160

 ctc ggc tcc tcc tgg tcc tac cag gtg ctc gcc acc gag ggc tac cag 528
 Leu Gly Ser Ser Trp Ser Tyr Gln Val Leu Ala Thr Glu Gly Tyr Gln
 165 170 175

 tcc tcc ggc tac tcc aac gtg acc gtg tgg tga 561
 Ser Ser Gly Tyr Ser Asn Val Thr Val Trp
 180 185

 <210> 66
 <211> 186
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Synthetic Construct

 <400> 66
 Met Ala Ser Thr Asp Tyr Trp Gln Asn Trp Thr Asp Gly Gly Gly Thr
 1 5 10 15

60110USPCT1 Corrected SEQ LIST 2-2007.txt

Val Asn Ala Thr Asn Gly Ser Asp Gly Asn Tyr Ser Val Ser Trp Ser
20 25 30

Asn Cys Gly Asn Phe Val Val Gly Lys Gly Trp Thr Thr Gly Ser Ala
35 40 45

Thr Arg Val Ile Asn Tyr Asn Ala Gly Ala Phe Ser Pro Ser Gly Asn
50 55 60

Gly Tyr Leu Ala Leu Tyr Gly Trp Thr Arg Asn Ser Leu Ile Glu Tyr
65 70 75 80

Tyr Val Val Asp Ser Trp Gly Thr Tyr Arg Pro Thr Gly Thr Tyr Lys
85 90 95

Gly Thr Val Thr Ser Asp Gly Gly Thr Tyr Asp Ile Tyr Thr Thr Thr
100 105 110

Arg Thr Asn Ala Pro Ser Ile Asp Gly Asn Asn Thr Thr Phe Thr Gln
115 120 125

Phe Trp Ser Val Arg Gln Ser Lys Arg Pro Ile Gly Thr Asn Asn Thr
130 135 140

Ile Thr Phe Ser Asn His Val Asn Ala Trp Lys Ser Lys Gly Met Asn
145 150 155 160

Leu Gly Ser Ser Trp Ser Tyr Gln Val Leu Ala Thr Glu Gly Tyr Gln
165 170 175

Ser Ser Gly Tyr Ser Asn Val Thr Val Trp
180 185

<210> 67
<211> 2071
<212> DNA
<213> Oryza sativa

<220>
<221> misc_feature
<222> (1)..(2071)
<223> Promoter

<400> 67
tccatgctgt cctactactt gcttcatccc cttctacatt ttgttctggt ttttggcctg 60
catttcggat catgatgtat gtgatttcca atctgctgca atatgaatgg agactctgtg 120
ctaaccatca acaacatgaa atgcttatga ggcctttgct gagcagccaa tcttgcctgt 180

60110USPCT1 Corrected SEQ LIST 2-2007.txt

gtttatgtct tcacaggccg aattcctctg ttttgttttt caccctcaat atttggaac	240
atttatctag gttgtttgtg tccaggccta taaatcatatc atgatgttgt cgtattggat	300
gtgaatgtgg tggcgtgttc agtgccttgg atttgagttt gatgagagtt gcttctgggt	360
caccactcac cattatcgat gctcctcttc agcataaggt aaaagtcttc cctgtttacg	420
ttattttacc cactatgggt gcttggggtg gttttttcct gattgcttat gccatggaaa	480
gtcatttgat atgttgaact tgaattaact gtagaattgt atacatgttc catttggtgt	540
gtacttcctt cttttctatt agtagcctca gatgagtggtg aaaaaaacag attatataac	600
ttgccctata aatcatttga aaaaaatatt gtacagtgtg aaattgatat atagtgaatt	660
tttaagagca tgttttccta aagaagtata ttttttctat gtacaaaggc cattgaagta	720
attgtagata caggataatg tagacttttt ggacttacac tgctaccttt aagtaacaat	780
catgagcaat agtgttgcaa tgatatttag gctgcattcg ttactctct tgatttccat	840
gagcacgctt cccaaactgt taaactctgt gttttttgcc aaaaaaaaaat gcataggaaa	900
gttgctttta aaaaatcata tcaatccatt ttttaagtta tagctaatac ttaattaatc	960
atgcgctaata agtcaactct gtttttcgta ctagagagat tgttttgaac cagcactcaa	1020
gaacacagcc ttaaccagc caaataatgc tacaacctac cagtccacac ctcttgtaaa	1080
gcatttggtg catggaaaag ctaagatgac agcaacctgt tcaggaaaac aactgacaag	1140
gtcatagggg gagggagctt ttggaaagggt gccgtgcagt tcaaacaatt agttagcagt	1200
agggtgttgg tttttgctca cagcaataag aagttaatca tgggtgtaggc aacccaaata	1260
aaacaccaaa atatgcacaa ggcagtttgt tgtattctgt agtacagaca aaactaaaag	1320
taatgaaaga agatgtggtg ttagaaaagg aaacaatatc atgagtaatg tgtgggcatt	1380
atgggaccac gaaataaaaa gaacattttg atgagtcgtg tatcctcgat gagcctcaaa	1440
agttctctca ccccgataa gaaaccctta agcaatgtgc aaagtttgca ttctccactg	1500
acataatgca aaataagata tcatcgatga catagcaact catgcatcat atcatgcctc	1560
tctcaaccta ttcattccta ctcatctaca taagtatctt cagctaaatg ttagaacata	1620
aacccataag tcacgtttga tgagtattag gcgtgacaca tgacaaatca cagactcaag	1680
caagataaag caaaatgatg tgtacataaa actccagagc tatatgtcat attgcaaaaa	1740
gaggagagct tataagacaa ggcagtactc acaaaaattc atttgccctt cgtgtcaaaa	1800
agaggagggc ttacattat ccatgtcata ttgcaaaaga aagagagaaa gaacaacaca	1860
atgctgcgtc aattatacat atctgtatgt ccatcattat tcatccacct ttcgtgtacc	1920
acacttcata tatcatgagt cacttcatgt ctggacatta acaactcta tcttaacatt	1980
tagatgcaag agcctttatc tcactataaa tgcacgatga tttctcattg tttctcacia	2040
aaagcattca gttcattagt cctacaacaa c	2071

60110USPCT1 Corrected SEQ LIST 2-2007.txt

<210> 68
 <211> 79
 <212> PRT
 <213> Zea mays

<220>
 <221> SIGNAL
 <222> (1)..(79)
 <223> Maize waxy signal sequence.

<400> 68

Met Leu Ala Ala Leu Ala Thr Ser Gln Leu Val Ala Thr Arg Ala Gly
 1 5 10 15

Leu Gly Val Pro Asp Ala Ser Thr Phe Arg Arg Gly Ala Ala Gln Gly
 20 25 30

Leu Arg Gly Ala Arg Ala Ser Ala Ala Ala Asp Thr Leu Ser Met Arg
 35 40 45

Thr Ser Ala Arg Ala Ala Pro Arg His Gln His Gln Gln Ala Arg Arg
 50 55 60

Gly Ala Arg Phe Pro Ser Leu Val Val Cys Ala Ser Ala Gly Ala
 65 70 75

<210> 69
 <211> 1005
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Bromelain Sequence

<220>
 <221> CDS
 <222> (1)..(1005)
 <223> Synthetic Bromelain

<400> 69

atg gcc tgg aag gtg cag gtg gtg ttc ctc ttc ctc ttc ctc tgc gtg 48
 Met Ala Trp Lys Val Gln Val Val Phe Leu Phe Leu Phe Leu Cys Val
 1 5 10 15

atg tgg gcc tcc ccg tcc gcc gcc tcc gcg gac gag ccg tcc gac ccg 96
 Met Trp Ala Ser Pro Ser Ala Ala Ser Ala Asp Glu Pro Ser Asp Pro
 20 25 30

atg atg aag cgc ttc gag gag tgg atg gtg gag tac ggc cgc gtg tac 144
 Met Met Lys Arg Phe Glu Glu Trp Met Val Glu Tyr Gly Arg Val Tyr
 35 40 45

aag gac aac gac gag aag atg cgc cgc ttc cag atc ttc aag aac aac 192

60110USPCT1 Corrected SEQ LIST 2-2007.txt

Lys	Asp	Asn	Asp	Glu	Lys	Met	Arg	Arg	Phe	Gln	Ile	Phe	Lys	Asn	Asn		
50					55					60							
gtg	aac	cac	atc	gag	acc	ttc	aac	tcc	cgc	aac	gag	aac	tcc	tac	acc	240	
Val	Asn	His	Ile	Glu	Thr	Phe	Asn	Ser	Arg	Asn	Glu	Asn	Ser	Tyr	Thr		
65				70					75					80			
ctc	ggc	atc	aac	cag	ttc	acc	gac	atg	acc	aac	aac	gag	ttc	atc	gcc	288	
Leu	Gly	Ile	Asn	Gln	Phe	Thr	Asp	Met	Thr	Asn	Asn	Glu	Phe	Ile	Ala		
				85					90					95			
cag	tac	acc	ggc	ggc	atc	tcc	cgc	ccg	ctc	aac	atc	gag	cgc	gag	ccg	336	
Gln	Tyr	Thr	Gly	Gly	Ile	Ser	Arg	Pro	Leu	Asn	Ile	Glu	Arg	Glu	Pro		
			100					105				110					
gtg	gtg	tcc	ttc	gac	gac	gtg	gac	atc	tcc	gcc	gtg	ccg	cag	tcc	atc	384	
Val	Val	Ser	Phe	Asp	Asp	Val	Asp	Ile	Ser	Ala	Val	Pro	Gln	Ser	Ile		
		115				120						125					
gac	tgg	cgc	gac	tac	ggc	gcc	gtg	acc	tcc	gtg	aag	aac	cag	aac	ccg	432	
Asp	Trp	Arg	Asp	Tyr	Gly	Ala	Val	Thr	Ser	Val	Lys	Asn	Gln	Asn	Pro		
	130					135					140						
tgc	ggc	gcc	tgc	tgg	gcc	ttc	gcc	gcc	atc	gcc	acc	gtg	gag	tcc	atc	480	
Cys	Gly	Ala	Cys	Trp	Ala	Phe	Ala	Ala	Ile	Ala	Thr	Val	Glu	Ser	Ile		
	145				150				155					160			
tac	aag	atc	aag	aag	ggc	atc	ctc	gag	ccg	ctc	tcc	gag	cag	cag	gtg	528	
Tyr	Lys	Ile	Lys	Lys	Gly	Ile	Leu	Glu	Pro	Leu	Ser	Glu	Gln	Gln	Val		
				165					170					175			
ctc	gac	tgc	gcc	aag	ggc	tac	ggc	tgc	aag	ggc	ggc	tgg	gag	ttc	cgc	576	
Leu	Asp	Cys	Ala	Lys	Gly	Tyr	Gly	Cys	Lys	Gly	Gly	Trp	Glu	Phe	Arg		
			180					185					190				
gcc	ttc	gag	ttc	atc	atc	tcc	aac	aag	ggc	gtg	gcc	tcc	ggc	gcc	atc	624	
Ala	Phe	Glu	Phe	Ile	Ile	Ser	Asn	Lys	Gly	Val	Ala	Ser	Gly	Ala	Ile		
		195				200						205					
tac	ccg	tac	aag	gcc	gcc	aag	ggc	acc	tgc	aag	acc	gac	ggc	gtg	ccg	672	
Tyr	Pro	Tyr	Lys	Ala	Ala	Lys	Gly	Thr	Cys	Lys	Thr	Asp	Gly	Val	Pro		
	210					215					220						
aac	tcc	gcc	tac	atc	acc	ggc	tac	gcc	cgc	gtg	ccg	cgc	aac	aac	gag	720	
Asn	Ser	Ala	Tyr	Ile	Thr	Gly	Tyr	Ala	Arg	Val	Pro	Arg	Asn	Asn	Glu		
	225				230					235					240		
tcc	tcc	atg	atg	tac	gcc	gtg	tcc	aag	cag	ccg	atc	acc	gtg	gcc	gtg	768	
Ser	Ser	Met	Met	Tyr	Ala	Val	Ser	Lys	Gln	Pro	Ile	Thr	Val	Ala	Val		
				245					250					255			
gac	gcc	aac	gcc	aac	ttc	cag	tac	tac	aag	tcc	ggc	gtg	ttc	aac	ggc	816	
Asp	Ala	Asn	Ala	Asn	Phe	Gln	Tyr	Tyr	Lys	Ser	Gly	Val	Phe	Asn	Gly		
			260				265						270				
ccg	tgc	ggc	acc	tcc	ctc	aac	cac	gcc	gtg	acc	gcc	atc	ggc	tac	ggc	864	
Pro	Cys	Gly	Thr	Ser	Leu	Asn	His	Ala	Val	Thr	Ala	Ile	Gly	Tyr	Gly		
		275					280					285					
cag	gac	tcc	atc	atc	tac	ccg	aag	aag	tgg	ggc	gcc	aag	tgg	ggc	gag	912	
Gln	Asp	Ser	Ile	Ile	Tyr	Pro	Lys	Lys	Trp	Gly	Ala	Lys	Trp	Gly	Glu		
	290					295					300						

60110USPCT1 Corrected SEQ LIST 2-2007.txt

gcc ggc tac atc cgc atg gcc cgc gac gtg tcc tcc tcc tcc ggc atc 960
 Ala Gly Tyr Ile Arg Met Ala Arg Asp Val Ser Ser Ser Ser Gly Ile
 305 310 315 320

tgc ggc atc gcc atc gac ccg ctc tac ccg acc ctc gag gag tag 1005
 Cys Gly Ile Ala Ile Asp Pro Leu Tyr Pro Thr Leu Glu Glu
 325 330

<210> 70

<211> 334

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 70

Met Ala Trp Lys Val Gln Val Val Phe Leu Phe Leu Phe Leu Cys Val
 1 5 10 15

Met Trp Ala Ser Pro Ser Ala Ala Ser Ala Asp Glu Pro Ser Asp Pro
 20 25 30

Met Met Lys Arg Phe Glu Glu Trp Met Val Glu Tyr Gly Arg Val Tyr
 35 40 45

Lys Asp Asn Asp Glu Lys Met Arg Arg Phe Gln Ile Phe Lys Asn Asn
 50 55 60

Val Asn His Ile Glu Thr Phe Asn Ser Arg Asn Glu Asn Ser Tyr Thr
 65 70 75 80

Leu Gly Ile Asn Gln Phe Thr Asp Met Thr Asn Asn Glu Phe Ile Ala
 85 90 95

Gln Tyr Thr Gly Gly Ile Ser Arg Pro Leu Asn Ile Glu Arg Glu Pro
 100 105 110

Val Val Ser Phe Asp Asp Val Asp Ile Ser Ala Val Pro Gln Ser Ile
 115 120 125

Asp Trp Arg Asp Tyr Gly Ala Val Thr Ser Val Lys Asn Gln Asn Pro
 130 135 140

Cys Gly Ala Cys Trp Ala Phe Ala Ala Ile Ala Thr Val Glu Ser Ile
 145 150 155 160

Tyr Lys Ile Lys Lys Gly Ile Leu Glu Pro Leu Ser Glu Gln Gln Val
 165 170 175

60110USPCT1 Corrected SEQ LIST 2-2007.txt

Leu Asp Cys Ala Lys Gly Tyr Gly Cys Lys Gly Gly Trp Glu Phe Arg
180 185 190

Ala Phe Glu Phe Ile Ile Ser Asn Lys Gly Val Ala Ser Gly Ala Ile
195 200 205

Tyr Pro Tyr Lys Ala Ala Lys Gly Thr Cys Lys Thr Asp Gly Val Pro
210 215 220

Asn Ser Ala Tyr Ile Thr Gly Tyr Ala Arg Val Pro Arg Asn Asn Glu
225 230 235 240

Ser Ser Met Met Tyr Ala Val Ser Lys Gln Pro Ile Thr Val Ala Val
245 250 255

Asp Ala Asn Ala Asn Phe Gln Tyr Tyr Lys Ser Gly Val Phe Asn Gly
260 265 270

Pro Cys Gly Thr Ser Leu Asn His Ala Val Thr Ala Ile Gly Tyr Gly
275 280 285

Gln Asp Ser Ile Ile Tyr Pro Lys Lys Trp Gly Ala Lys Trp Gly Glu
290 295 300

Ala Gly Tyr Ile Arg Met Ala Arg Asp Val Ser Ser Ser Ser Gly Ile
305 310 315 320

Cys Gly Ile Ala Ile Asp Pro Leu Tyr Pro Thr Leu Glu Glu
325 330

<210> 71
<211> 78
<212> DNA
<213> Artificial Sequence

<220>
<223> Bromealin signal sequence

<400> 71
atggcctgga aggtgcaggt ggtgttcctc ttcctcttcc tctgcgtgat gtgggcctcc 60
ccgtccgccg cctccgcc 78

<210> 72
<211> 26
<212> PRT
<213> Artificial Sequence

<220>
<223> Bromealin signal peptide

<400> 72

60110USPCT1 Corrected SEQ LIST 2-2007.txt

Met Ala Trp Lys Val Gln Val Val Phe Leu Phe Leu Phe Leu Cys Val
1 5 10 15

Met Trp Ala Ser Pro Ser Ala Ala Ser Ala
20 25

<210> 73
<211> 1050
<212> DNA
<213> Artificial Sequence

<220>
<223> pSYN11000

<400> 73
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ccgtccgccg cctccgcgga cgagccgtcc gacccgatga tgaagcgctt cgaggagtgg 120
atggtggagt acggccgcgt gtacaaggac aacgacgaga agatgcgccg cttccagatc 180
ttcaagaaca acgtgaacca catcgagacc ttcaactccc gcaacgagaa ctctacacc 240
ctcggcatca accagttcac cgacatgacc aacaacgagt tcatcgccca gtacaccggc 300
ggcatctccc gcccgtcaa catcgagcgc gagccggtgg tgtccttcga cgacgtggac 360
atctccgccg tgccgcagtc catcgactgg cgcgactacg gcgccgtgac ctccgtgaag 420
aaccagaacc cgtgcggcgc ctgctgggcc ttccgcccca tcgccaccgt ggagtccatc 480
tacaagatca agaagggcat cctcgagccg ctctccgagc agcaggtgct cgactgcgcc 540
aagggctacg gctgcaaggg cggtgaggag ttccgcgcct tcgagttcat catctccaac 600
aagggcgtgg cctccggcgc catctacccg tacaaggccg ccaagggcac ctgcaagacc 660
gacggcgtgc cgaactccgc ctacatcacc ggctacgcc gcgtgccgcg caacaacgag 720
tcctccatga tgtacgccgt gtccaagcag ccgatcaccg tggccgtgga cgccaacgcc 780
aacttccagt actacaagtc cggcgtgttc aacggcccgt gcggcacctc cctcaaccac 840
gccgtgaccg ccatcggcta cggccaggac tccatcatct acccgaagaa gtggggcgcc 900
aagtggggcg aggccggcta catccgcatg gcccgcgacg tgtcctctc ctccggcatc 960
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gccgccaact ccaccctcgt ggccgagtag 1050

<210> 74
<211> 1067
<212> DNA
<213> Artificial Sequence

<220>
<223> pSYN11589

60110USPCT1 Corrected SEQ LIST 2-2007.txt

<400> 74

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ccgaccgcgc cgcctccacc gacgagccgt ccgacccgat gatgaagcgc ttcgaggagt      180
ggatggtgga gtacggccgc gtgtacaagg acaacgacga gaagatgcgc cgcttcacaga      240
tcttcaagaa caacgtgaac cacatcgaga ctttcaactc ccgcaacgag aactcctaca      300
ccctcggcat caaccagttc accgacatga ccaacaacga gttcacgcc cagtacaccg      360
gcggcatctc ccgcccgtc aacatcgagc gcgagccggt ggtgtccttc gacgacgtgg      420
acatctccgc cgtgccgcag tccatcgact ggccgcgacta cggcgccgtg acctccgtga      480
agaaccagaa cccgtgcggc gcctgctggg ccttcgccgc catcgccacc gtggagtcca      540
tctacaagat caagaagggc atcctcgagc cgctctccga gcagcaggtg ctcgactgcg      600
ccaagggcta cggctgcaag ggcggctggg agttccgcgc cttcgagttc atcatctcca      660
acaagggcgt ggcctccggc gccatctacc cgtacaaggc cgccaagggc acctgcaaga      720
ccgacggcgt gccgaactcc gcctacatca ccggctacgc ccgctgcccg cgcaacaacg      780
agtctcccat gatgtacgcc gtgtccaagc agccgatcac cgtggccgtg gacgccaacg      840
ccaacttcca gtactacaag tccggcgtgt tcaacggccc gtgcggcacc tccctcaacc      900
acgccgtgac cgccatcggc tacggccagg actccatcat ctaccgaag aagtggggcg      960
ccaagtgggg cgaggccggc tacatccgca tggcccgcga cgtgtcctcc tcctccggca     1020
tctgcggcat cgccatcgac ccgctctacc cgaccctcga ggagtag                       1067

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<210> 75

<211> 1023

<212> DNA

<213> Artificial Sequence

<220>

<223> pSYN11587 Sequence

<400> 75

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ccgtccgccg cctccgcgga cgagccgtcc gacccgatga tgaagcgctt cgaggagtgg      120
atggtggagt acggccgcgt gtacaaggac aacgacgaga agatgcgccg cttccagatc      180
ttcaagaaca acgtgaacca catcgagacc ttcaactccc gcaacgagaa ctcctacacc      240
ctcggcatca accagttcac cgacatgacc aacaacgagt tcatcgccca gtacaccggc      300
ggcatctccc gcccgtcaa catcgagcgc gagccggtgg tgtccttcga cgacgtggac      360
atctccgccg tgccgcagtc catcgactgg cgcgactacg gcgccgtgac ctccgtgaag      420
aaccagaacc cgtgcggcgc ctgctggggc ttcgccgcca tcgccaccgt ggagtccatc      480

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60110USPCT1 Corrected SEQ LIST 2-2007.txt

tacaagatca agaagggcat cctcgagccg ctctccgagc agcaggtgct cgactgcgcc	540
aagggctacg gctgcaaggc cggctgggag ttccgcgcct tcgagttcat catctccaac	600
aagggcgtgg cctccggcgc catctacccg tacaaggccg ccaagggcac ctgcaagacc	660
gacggcgtgc cgaactccgc ctacatcacc ggctacgccc gcgtgccgcg caacaacgag	720
tcctccatga tgtacgccgt gtccaagcag ccgatcaccg tggccgtgga cgccaacgcc	780
aacttccagt actacaagtc cggcgtgttc aacggcccgt gcggcacctc cctcaaccac	840
gccgtgaccg ccatcggtta cggccaggac tccatcatct acccgaagaa gtggggcgcc	900
aagtggggcg aggccggcta catccgcatg gcccgcgacg tgcctcctc ctccggcatc	960
tgccggcatcg ccatcgaccc gctctacccg accctcgagg agtccgagaa ggacgagctg	1020
tag	1023

<210> 76

<211> 990

<212> DNA

<213> Artificial Sequence

<220>

<223> pSYN12169 Sequence

<400> 76

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gcggacgagc cgtccgaccc gatgatgaag cgcttcgagg agtggatggg ggagtacggc	120
cgcggtgtaca aggacaacga cgagaagatg cgccgcttcc agatcttcaa gaacaacgtg	180
aaccacatcg agaccttcaa ctcccgaac gagaactcct acaccctcgg catcaaccag	240
ttcaccgaca tgaccaacaa cgagttcatc gcccagtaca ccggcgggcat ctcccgcccg	300
ctcaacatcg agcgcgagcc ggtgggtgtcc ttcgacgacg tggacatctc cgccgtgccg	360
cagtccatcg actggcgcca ctacggcgcc gtgacctccg tgaagaacca gaacccgtgc	420
ggcgccctgct gggccttcgc cgccatcgcc accgtggagt ccatctacaa gatcaagaag	480
ggcatcctcg agccgctctc cgagcagcag gtgctcgact gcgccaaggg ctacggctgc	540
aagggcggct gggagtccg cgcttcgag ttcatcatct ccaacaaggg cgtggcctcc	600
ggcgccatct acccgtaaa ggccgccaag ggcacctgca agaccgacgg cgtgccgaac	660
tccgcctaca tcaccggcta cgcccgctg ccgcgcaaca acgagtcctc catgatgtac	720
gccgtgtcca agcagccgat caccgtggcc gtggacgcca acgccaactt ccagtactac	780
aagtccggcg tgttcaacgg cccgtgcggc acctccctca accacgccgt gaccgccatc	840
ggctacggcc aggactccat catctacccg aagaagtggg gcgccaagtg gggcgaggcc	900
ggctacatcc gcatggcccg cgacgtgtcc tcctcctccg gcatctgcgg catcgccatc	960
gacccgctct acccgaccct cgaggagtag	990

60110USPCT1 Corrected SEQ LIST 2-2007.txt

<210> 77
 <211> 1170
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> pSYN12575 Sequence

<400> 77
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 gacgcgtcca cgttccgccg cggcgccgcg cagggcctga ggggggccccg ggcgtcggcg 120
 gcggcggaca cgctcagcat gcggaccagc gcgcgcgcgg cgcccaggca ccagcaccag 180
 caggcgcgcc gcggggccag gttcccgtcg ctcgtcgtgt gcgccagcgc cggcgccatg 240
 gcggacgagc cgtccgaccc gatgatgaag cgcttcgagg agtggatggt ggagtacggc 300
 cgcggtgtaca aggacaacga cgagaagatg cgccgcttcc agatcttcaa gaacaacgtg 360
 aaccacatcg agaccttcaa ctcccgaac gagaactcct acaccctcgg catcaaccag 420
 ttcaccgaca tgaccaacaa cgagttcatc gcccagtaca ccggcgggcat ctcccgccccg 480
 ctcaacatcg agcgcgagcc ggtggtgtcc ttcgacgacg tggacatctc cgccgtgccg 540
 cagtccatcg actggcgcgga ctacggcgcc gtgacctccg tgaagaacca gaacccgtgc 600
 ggcgcctgct gggccttcgc cgccatcgcc accgtggagt ccatctacaa gatcaagaag 660
 ggcacacctg agccgctctc cgagcagcag gtgctcgact gcgccaaggg ctacggctgc 720
 aagggcggct gggagttccg cgccttcgag ttcatcatct ccaacaaggg cgtggcctcc 780
 ggcgccatct acccgtagaa ggccgccaag ggcacctgca agaccgacgg cgtgccgaac 840
 tccgcctaca tcaccggcta cgcccgcggt ccgcgcaaca acgagtcctc catgatgtac 900
 gccgtgtcca agcagccgat caccgtggcc gtggacgcca acgccaactt ccagtactac 960
 aagtccggcg tgttcaacgg cccgtgcggc acctccctca accacgccgt gaccgccatc 1020
 ggctacggcc aggactccat catctacccg aagaagtggg gcgccaagtg gggcgaggcc 1080
 ggctacatcc gcatggcccc cgacgtgtcc tcctcctccg gcatctgcgg catcgccatc 1140
 gacccgctct acccgaccct cgaggagtag 1170

<210> 78
 <211> 1068
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> pSM270 Sequence

<400> 78
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60110USPCT1 Corrected SEQ LIST 2-2007.txt

ccgtccgccg cctccgcctc ctcctcctcc ttcgccgact ccaacccgat ccgcccgggtg	120
accgaccgcg ccgcctccac cgacgagccg tccgacccga tgatgaagcg cttcgaggag	180
tggatggtgg agtacggccg cgtgtacaag gacaacgacg agaagatgcg ccgcttccag	240
atcttcaaga acaacgtgaa ccacatcgag accttcaact cccgcaacga gaactcctac	300
accctcggca tcaaccagtt caccgacatg accaacaacg agttcatcgc ccagtacacc	360
ggcggcacat cccgcccgt caacatcgag cgcgagccgg tgggtgcctt cgacgacgtg	420
gacatctccg ccgtgccgca gtccatcgac tggcgcgact acggcgccgt gacctccgtg	480
aagaaccaga acccgtgcgg cgcctgctgg gccttcgccg ccatcgccac cgtggagtcc	540
atctacaaga tcaagaaggg catcctcgag ccgctctccg agcagcaggt gctcgactgc	600
gccaagggct acggctgcaa gggcggctgg gagttccgcg ccttcgagtt catcatctcc	660
aacaagggcg tggcctccgg cgccatctac ccgtacaagg ccgccaaggg cacctgcaag	720
accgacggcg tgccgaactc cgcctacatc accggctacg cccgcgtgcc gcgcaacaac	780
gagtcctcca tgatgtacgc cgtgtccaag cagccgatca ccgtggccgt ggacgccaac	840
gccaacttcc agtactacaa gtccggcgtg ttcaacggcc cgtgcggcac ctccctcaac	900
cacgccgtga ccgccatcgg ctacggccag gactccatca tctacccgaa gaagtggggc	960
gccaagtggg gcgaggccgg ctacatccgc atggcccgcg acgtgtcctc ctcctccggc	1020
atctgcggca tcgccatcga cccgctctac ccgaccctcg aggagtag	1068

<210> 79
 <211> 1497
 <212> DNA
 <213> *Trichoderma reesei*

<220>
 <221> CDS
 <222> (1)..(1497)
 <223> *Trichoderma reesei* cellobiohydrolase I

<400> 79	
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1 5 10 15	
tgg cag aaa tgc tcg tct ggt ggc acg tgc act caa cag aca ggc tcc	96
Trp Gln Lys Cys Ser Ser Gly Gly Thr Cys Thr Gln Gln Thr Gly Ser	
20 25 30	
gtg gtc atc gac gcc aac tgg cgc tgg act cac gct acg aac agc agc	144
Val Val Ile Asp Ala Asn Trp Arg Trp Thr His Ala Thr Asn Ser Ser	
35 40 45	
acg aac tgc tac gat ggc aac act tgg agc tcg acc cta tgt cct gac	192
Thr Asn Cys Tyr Asp Gly Asn Thr Trp Ser Ser Thr Leu Cys Pro Asp	
50 55 60	

60110USPCT1 Corrected SEQ LIST 2-2007.txt

aac gag acc tgc gcg aag aac tgc tgt ctg gac ggt gcc gcc tac gcg Asn Glu Thr Cys Ala Lys Asn Cys Cys Leu Asp Gly Ala Ala Tyr Ala 65 70 75 80	240
tcc acg tac gga gtt acc acg agc ggt aac agc ctc tcc att ggc ttt Ser Thr Tyr Gly Val Thr Thr Ser Gly Asn Ser Leu Ser Ile Gly Phe 85 90 95	288
gtc acc cag tct gcg cag aag aac gtt ggc gct cgc ctt tac ctt atg Val Thr Gln Ser Ala Gln Lys Asn Val Gly Ala Arg Leu Tyr Leu Met 100 105 110	336
gcg agc gac acg acc tac cag gaa ttc acc ctg ctt ggc aac gag ttc Ala Ser Asp Thr Thr Tyr Gln Glu Phe Thr Leu Leu Gly Asn Glu Phe 115 120 125	384
tct ttc gat gtt gat gtt tcg cag ctg ccg tgc ggc ttg aac gga gct Ser Phe Asp Val Asp Val Ser Gln Leu Pro Cys Gly Leu Asn Gly Ala 130 135 140	432
ctc tac ttc gtg tcc atg gac gcg gat ggt ggc gtg agc aag tat ccc Leu Tyr Phe Val Ser Met Asp Ala Asp Gly Gly Val Ser Lys Tyr Pro 145 150 155 160	480
acc aac acc gct ggc gcc aag tac ggc acg ggg tac tgt gac agc cag Thr Asn Thr Ala Gly Ala Lys Tyr Gly Thr Gly Tyr Cys Asp Ser Gln 165 170 175	528
tgt ccc cgc gat ctg aag ttc atc aat ggc cag gcc aac gtt gag ggc Cys Pro Arg Asp Leu Lys Phe Ile Asn Gly Gln Ala Asn Val Glu Gly 180 185 190	576
tgg gag ccg tca tcc aac aac gcg aac acg ggc att gga gga cac gga Trp Glu Pro Ser Ser Asn Asn Ala Asn Thr Gly Ile Gly Gly His Gly 195 200 205	624
agc tgc tgc tct gag atg gat atc tgg gag gcc aac tcc atc tcc gag Ser Cys Cys Ser Glu Met Asp Ile Trp Glu Ala Asn Ser Ile Ser Glu 210 215 220	672
gct ctt acc ccc cac cct tgc acg act gtc ggc cag gag atc tgc gag Ala Leu Thr Pro His Pro Cys Thr Thr Val Gly Gln Glu Ile Cys Glu 225 230 235 240	720
ggt gat ggg tgc ggc gga act tac tcc gat aac aga tat ggc ggc act Gly Asp Gly Cys Gly Gly Thr Tyr Ser Asp Asn Arg Tyr Gly Gly Thr 245 250 255	768
tgc gat ccc gat ggc tgc gac tgg aac cca tac cgc ctg ggc aac acc Cys Asp Pro Asp Gly Cys Asp Trp Asn Pro Tyr Arg Leu Gly Asn Thr 260 265 270	816
agc ttc tac ggc cct ggc tct agc ttt acc ctc gat acc acc aag aaa Ser Phe Tyr Gly Pro Gly Ser Ser Phe Thr Leu Asp Thr Thr Lys Lys 275 280 285	864
ttg acc gtt gtc acc cag ttc gag acg tcg ggt gcc atc aac cga tac Leu Thr Val Val Thr Gln Phe Glu Thr Ser Gly Ala Ile Asn Arg Tyr 290 295 300	912
tat gtc cag aat ggc gtc act ttc cag cag ccc aac gcc gag ctt ggt Tyr Val Gln Asn Gly Val Thr Phe Gln Gln Pro Asn Ala Glu Leu Gly 305 310 315 320	960

60110USPCT1 Corrected SEQ LIST 2-2007.txt

agt tac tct ggc aac gag ctc aac gat gat tac tgc aca gct gag gag	1008
Ser Tyr Ser Gly Asn Glu Leu Asn Asp Asp Tyr Cys Thr Ala Glu Glu	
325 330 335	
gca gaa ttc ggc gga tcc tct ttc tca gac aag ggc ggc ctg act cag	1056
Ala Glu Phe Gly Gly Ser Ser Phe Ser Asp Lys Gly Gly Leu Thr Gln	
340 345 350	
ttc aag aag gct acc tct ggc ggc atg gtt ctg gtc atg agt ctg tgg	1104
Phe Lys Lys Ala Thr Ser Gly Gly Met Val Leu Val Met Ser Leu Trp	
355 360 365	
gat gat tac tac gcc aac atg ctg tgg ctg gac tcc acc tac ccg aca	1152
Asp Asp Tyr Tyr Ala Asn Met Leu Trp Leu Asp Ser Thr Tyr Pro Thr	
370 375 380	
aac gag acc tcc tcc aca ccc ggt gcc gtg cgc gga agc tgc tcc acc	1200
Asn Glu Thr Ser Ser Thr Pro Gly Ala Val Arg Gly Ser Cys Ser Thr	
385 390 395 400	
agc tcc ggt gtc cct gct cag gtc gaa tct cag tct ccc aac gcc aag	1248
Ser Ser Gly Val Pro Ala Gln Val Glu Ser Gln Ser Pro Asn Ala Lys	
405 410 415	
gtc acc ttc tcc aac atc aag ttc gga ccc att ggc agc acc ggc aac	1296
Val Thr Phe Ser Asn Ile Lys Phe Gly Pro Ile Gly Ser Thr Gly Asn	
420 425 430	
cct agc ggc ggc aac cct ccc ggc gga aac ccg cct ggc acc acc acc	1344
Pro Ser Gly Gly Asn Pro Pro Gly Gly Asn Pro Pro Gly Thr Thr Thr	
435 440 445	
acc cgc cgc cca gcc act acc act gga agc tct ccc gga cct acc cag	1392
Thr Arg Arg Pro Ala Thr Thr Thr Gly Ser Ser Pro Gly Pro Thr Gln	
450 455 460	
tct cac tac ggc cag tgc ggc ggt att ggc tac agc ggc ccc acg gtc	1440
Ser His Tyr Gly Gln Cys Gly Gly Ile Gly Tyr Ser Gly Pro Thr Val	
465 470 475 480	
tgc gcc agc ggc aca act tgc cag gtc ctg aac cct tac tac tct cag	1488
Cys Ala Ser Gly Thr Thr Cys Gln Val Leu Asn Pro Tyr Tyr Ser Gln	
485 490 495	
tgc ctg taa	1497
Cys Leu	

<210> 80

<211> 498

<212> PRT

<213> Trichoderma reesei

<400> 80

Met Gln Ser Ala Cys Thr Leu Gln Ser Glu Thr His Pro Pro Leu Thr
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Trp Gln Lys Cys Ser Ser Gly Gly Thr Cys Thr Gln Gln Thr Gly Ser
20 25 30

60110USPCT1 Corrected SEQ LIST 2-2007.txt

Val Val Ile Asp Ala Asn Trp Arg Trp Thr His Ala Thr Asn Ser Ser
 35 40 45
 Thr Asn Cys Tyr Asp Gly Asn Thr Trp Ser Ser Thr Leu Cys Pro Asp
 50 55 60
 Asn Glu Thr Cys Ala Lys Asn Cys Cys Leu Asp Gly Ala Ala Tyr Ala
 65 70 75 80
 Ser Thr Tyr Gly Val Thr Thr Ser Gly Asn Ser Leu Ser Ile Gly Phe
 85 90 95
 Val Thr Gln Ser Ala Gln Lys Asn Val Gly Ala Arg Leu Tyr Leu Met
 100 105 110
 Ala Ser Asp Thr Thr Tyr Gln Glu Phe Thr Leu Leu Gly Asn Glu Phe
 115 120 125
 Ser Phe Asp Val Asp Val Ser Gln Leu Pro Cys Gly Leu Asn Gly Ala
 130 135 140
 Leu Tyr Phe Val Ser Met Asp Ala Asp Gly Gly Val Ser Lys Tyr Pro
 145 150 155 160
 Thr Asn Thr Ala Gly Ala Lys Tyr Gly Thr Gly Tyr Cys Asp Ser Gln
 165 170 175
 Cys Pro Arg Asp Leu Lys Phe Ile Asn Gly Gln Ala Asn Val Glu Gly
 180 185 190
 Trp Glu Pro Ser Ser Asn Asn Ala Asn Thr Gly Ile Gly Gly His Gly
 195 200 205
 Ser Cys Cys Ser Glu Met Asp Ile Trp Glu Ala Asn Ser Ile Ser Glu
 210 215 220
 Ala Leu Thr Pro His Pro Cys Thr Thr Val Gly Gln Glu Ile Cys Glu
 225 230 235 240
 Gly Asp Gly Cys Gly Gly Thr Tyr Ser Asp Asn Arg Tyr Gly Gly Thr
 245 250 255
 Cys Asp Pro Asp Gly Cys Asp Trp Asn Pro Tyr Arg Leu Gly Asn Thr
 260 265 270
 Ser Phe Tyr Gly Pro Gly Ser Ser Phe Thr Leu Asp Thr Thr Lys Lys
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280

285

Leu Thr Val Val Thr Gln Phe Glu Thr Ser Gly Ala Ile Asn Arg Tyr
 290 295 300

Tyr Val Gln Asn Gly Val Thr Phe Gln Gln Pro Asn Ala Glu Leu Gly
 305 310 315 320

Ser Tyr Ser Gly Asn Glu Leu Asn Asp Asp Tyr Cys Thr Ala Glu Glu
 325 330 335

Ala Glu Phe Gly Gly Ser Ser Phe Ser Asp Lys Gly Gly Leu Thr Gln
 340 345 350

Phe Lys Lys Ala Thr Ser Gly Gly Met Val Leu Val Met Ser Leu Trp
 355 360 365

Asp Asp Tyr Tyr Ala Asn Met Leu Trp Leu Asp Ser Thr Tyr Pro Thr
 370 375 380

Asn Glu Thr Ser Ser Thr Pro Gly Ala Val Arg Gly Ser Cys Ser Thr
 385 390 395 400

Ser Ser Gly Val Pro Ala Gln Val Glu Ser Gln Ser Pro Asn Ala Lys
 405 410 415

Val Thr Phe Ser Asn Ile Lys Phe Gly Pro Ile Gly Ser Thr Gly Asn
 420 425 430

Pro Ser Gly Gly Asn Pro Pro Gly Gly Asn Pro Pro Gly Thr Thr Thr
 435 440 445

Thr Arg Arg Pro Ala Thr Thr Thr Gly Ser Ser Pro Gly Pro Thr Gln
 450 455 460

Ser His Tyr Gly Gln Cys Gly Gly Ile Gly Tyr Ser Gly Pro Thr Val
 465 470 475 480

Cys Ala Ser Gly Thr Thr Cys Gln Val Leu Asn Pro Tyr Tyr Ser Gln
 485 490 495

Cys Leu

<210> 81

<211> 1365

<212> DNA

<213> Trichoderma reesei

60110USPCT1 Corrected SEQ LIST 2-2007.txt

<220>

<221> CDS

<222> (1)..(1365)

<223> trichoderma reesei cellobiohydrolase II

<400> 81

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Met	Val	Pro	Leu	Glu	Glu	Arg	Gln	Ala	Cys	Ser	Ser	Val	Trp	Gly	Gln	
1				5				10						15		

tgt	ggt	ggc	cag	aat	tgg	tcg	ggt	ccg	act	tgc	tgt	gct	tcc	gga	agc	96
Cys	Gly	Gly	Gln	Asn	Trp	Ser	Gly	Pro	Thr	Cys	Cys	Ala	Ser	Gly	Ser	
			20					25					30			

aca	tgc	gtc	tac	tcc	aac	gac	tat	tac	tcc	cag	tgt	ctt	ccc	ggc	gct	144
Thr	Cys	Val	Tyr	Ser	Asn	Asp	Tyr	Tyr	Ser	Gln	Cys	Leu	Pro	Gly	Ala	
		35					40					45				

gca	agc	tca	agc	tcg	tcc	acg	cgc	gcc	gcg	tcg	acg	act	tca	cga	gta	192
Ala	Ser	Ser	Ser	Ser	Ser	Thr	Arg	Ala	Ala	Ser	Thr	Thr	Ser	Arg	Val	
	50					55					60					

tcc	ccc	aca	aca	tcc	cgg	tcg	agc	tcc	gcg	acg	cct	cca	cct	ggt	tct	240
Ser	Pro	Thr	Thr	Ser	Arg	Ser	Ser	Ser	Ala	Thr	Pro	Pro	Pro	Gly	Ser	
65					70					75				80		

acc	act	acc	aga	gta	cct	cca	gtc	gga	tcg	gga	acc	gct	acg	tat	tca	288
Thr	Thr	Thr	Arg	Val	Pro	Pro	Val	Gly	Ser	Gly	Thr	Ala	Thr	Tyr	Ser	
			85					90						95		

ggc	aac	cct	ttt	gtt	ggg	gtc	act	cct	tgg	gcc	aat	gca	tat	tac	gcc	336
Gly	Asn	Pro	Phe	Val	Gly	Val	Thr	Pro	Trp	Ala	Asn	Ala	Tyr	Tyr	Ala	
			100					105					110			

tct	gaa	gtt	agc	agc	ctc	gct	att	cct	agc	ttg	act	gga	gcc	atg	gcc	384
Ser	Glu	Val	Ser	Ser	Leu	Ala	Ile	Pro	Ser	Leu	Thr	Gly	Ala	Met	Ala	
		115					120					125				

act	gct	gca	gca	gct	gtc	gca	aag	gtt	ccc	tct	ttt	atg	tgg	cta	gat	432
Thr	Ala	Ala	Ala	Ala	Val	Ala	Lys	Val	Pro	Ser	Phe	Met	Trp	Leu	Asp	
	130					135					140					

act	ctt	gac	aag	acc	cct	ctc	atg	gag	caa	acc	ttg	gcc	gac	atc	cgc	480
Thr	Leu	Asp	Lys	Thr	Pro	Leu	Met	Glu	Gln	Thr	Leu	Ala	Asp	Ile	Arg	
145					150					155					160	

acc	gcc	aac	aag	aat	ggc	ggt	aac	tat	gcc	gga	cag	ttt	gtg	gtg	tat	528
Thr	Ala	Asn	Lys	Asn	Gly	Gly	Asn	Tyr	Ala	Gly	Gln	Phe	Val	Val	Tyr	
				165					170					175		

gac	ttg	ccg	gat	cgc	gat	tgc	gct	gcc	ctt	gcc	tcg	aat	ggc	gaa	tac	576
Asp	Leu	Pro	Asp	Arg	Asp	Cys	Ala	Ala	Leu	Ala	Ser	Asn	Gly	Glu	Tyr	
			180					185					190			

tct	att	gcc	gat	ggt	ggc	gtc	gcc	aaa	tat	aag	aac	tat	atc	gac	acc	624
Ser	Ile	Ala	Asp	Gly	Gly	Val	Ala	Lys	Tyr	Lys	Asn	Tyr	Ile	Asp	Thr	
		195					200					205				

att	cgt	caa	att	gtc	gtg	gaa	tat	tcc	gat	atc	cgg	acc	ctc	ctg	gtt	672
Ile	Arg	Gln	Ile	Val	Val	Glu	Tyr	Ser	Asp	Ile	Arg	Thr	Leu	Leu	Val	
	210					215					220					

60110USPCT1 Corrected SEQ LIST 2-2007.txt

att gag cct gac tct ctt gcc aac ctg gtg acc aac ctc ggt act cca Ile Glu Pro Asp Ser Leu Ala Asn Leu Val Thr Asn Leu Gly Thr Pro 225 230 235 240	720
aag tgt gcc aat gct cag tca gcc tac ctt gag tgc atc aac tac gcc Lys Cys Ala Asn Ala Gln Ser Ala Tyr Leu Glu Cys Ile Asn Tyr Ala 245 250 255	768
gtc aca cag ctg aac ctt cca aat gtt gcg atg tat ttg gac gct ggc Val Thr Gln Leu Asn Leu Pro Asn Val Ala Met Tyr Leu Asp Ala Gly 260 265 270	816
cat gca gga tgg ctt ggc tgg ccg gca aac caa gac ccg gcc gct cag His Ala Gly Trp Leu Gly Trp Pro Ala Asn Gln Asp Pro Ala Ala Gln 275 280 285	864
cta ttt gca aat gtt tac aag aat gca tcg tct ccg aga gct ctt cgc Leu Phe Ala Asn Val Tyr Lys Asn Ala Ser Ser Pro Arg Ala Leu Arg 290 295 300	912
gga ttg gca acc aat gtc gcc aac tac aac ggg tgg aac att acc agc Gly Leu Ala Thr Asn Val Ala Asn Tyr Asn Gly Trp Asn Ile Thr Ser 305 310 315 320	960
ccc cca tcg tac acg caa ggc aac gct gtc tac aac gag aag ctg tac Pro Pro Ser Tyr Thr Gln Gly Asn Ala Val Tyr Asn Glu Lys Leu Tyr 325 330 335	1008
atc cac gct att gga cct ctt ctt gcc aat cac ggc tgg tcc aac gcc Ile His Ala Ile Gly Pro Leu Leu Ala Asn His Gly Trp Ser Asn Ala 340 345 350	1056
ttc ttc atc act gat caa ggt cga tcg gga aag cag cct acc gga cag Phe Phe Ile Thr Asp Gln Gly Arg Ser Gly Lys Gln Pro Thr Gly Gln 355 360 365	1104
caa cag tgg gga gac tgg tgc aat gtg atc ggc acc gga ttt ggt att Gln Gln Trp Gly Asp Trp Cys Asn Val Ile Gly Thr Gly Phe Gly Ile 370 375 380	1152
cgc cca tcc gca aac act ggg gac tcg ttg ctg gat tcg ttt gtc tgg Arg Pro Ser Ala Asn Thr Gly Asp Ser Leu Leu Asp Ser Phe Val Trp 385 390 395 400	1200
gtc aag cca ggc ggc gag tgt gac ggc acc agc gac agc agt gcg cca Val Lys Pro Gly Gly Glu Cys Asp Gly Thr Ser Asp Ser Ser Ala Pro 405 410 415	1248
cga ttt gac tcc cac tgt gcg ctc cca gat gcc ttg caa ccg gcg cct Arg Phe Asp Ser His Cys Ala Leu Pro Asp Ala Leu Gln Pro Ala Pro 420 425 430	1296
caa gct ggt gct tgg ttc caa gcc tac ttt gtg cag ctt ctc aca aac Gln Ala Gly Ala Trp Phe Gln Ala Tyr Phe Val Gln Leu Leu Thr Asn 435 440 445	1344
gca aac cca tcg ttc ctg tag Ala Asn Pro Ser Phe Leu 450	1365

60110USPCT1 Corrected SEQ LIST 2-2007.txt

<211> 454

<212> PRT

<213> Trichoderma reesei

<400> 82

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 1 5 10 15

Cys Gly Gly Gln Asn Trp Ser Gly Pro Thr Cys Cys Ala Ser Gly Ser
 20 25 30

Thr Cys Val Tyr Ser Asn Asp Tyr Tyr Ser Gln Cys Leu Pro Gly Ala
 35 40 45

Ala Ser Ser Ser Ser Ser Thr Arg Ala Ala Ser Thr Thr Ser Arg Val
 50 55 60

Ser Pro Thr Thr Ser Arg Ser Ser Ser Ala Thr Pro Pro Pro Gly Ser
 65 70 75 80

Thr Thr Thr Arg Val Pro Pro Val Gly Ser Gly Thr Ala Thr Tyr Ser
 85 90 95

Gly Asn Pro Phe Val Gly Val Thr Pro Trp Ala Asn Ala Tyr Tyr Ala
 100 105 110

Ser Glu Val Ser Ser Leu Ala Ile Pro Ser Leu Thr Gly Ala Met Ala
 115 120 125

Thr Ala Ala Ala Ala Val Ala Lys Val Pro Ser Phe Met Trp Leu Asp
 130 135 140

Thr Leu Asp Lys Thr Pro Leu Met Glu Gln Thr Leu Ala Asp Ile Arg
 145 150 155 160

Thr Ala Asn Lys Asn Gly Gly Asn Tyr Ala Gly Gln Phe Val Val Tyr
 165 170 175

Asp Leu Pro Asp Arg Asp Cys Ala Ala Leu Ala Ser Asn Gly Glu Tyr
 180 185 190

Ser Ile Ala Asp Gly Gly Val Ala Lys Tyr Lys Asn Tyr Ile Asp Thr
 195 200 205

Ile Arg Gln Ile Val Val Glu Tyr Ser Asp Ile Arg Thr Leu Leu Val
 210 215 220

Ile Glu Pro Asp Ser Leu Ala Asn Leu Val Thr Asn Leu Gly Thr Pro
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Lys Cys Ala Asn Ala Gln Ser Ala Tyr Leu Glu Cys Ile Asn Tyr Ala
245 250 255

Val Thr Gln Leu Asn Leu Pro Asn Val Ala Met Tyr Leu Asp Ala Gly
260 265 270

His Ala Gly Trp Leu Gly Trp Pro Ala Asn Gln Asp Pro Ala Ala Gln
275 280 285

Leu Phe Ala Asn Val Tyr Lys Asn Ala Ser Ser Pro Arg Ala Leu Arg
290 295 300

Gly Leu Ala Thr Asn Val Ala Asn Tyr Asn Gly Trp Asn Ile Thr Ser
305 310 315 320

Pro Pro Ser Tyr Thr Gln Gly Asn Ala Val Tyr Asn Glu Lys Leu Tyr
325 330 335

Ile His Ala Ile Gly Pro Leu Leu Ala Asn His Gly Trp Ser Asn Ala
340 345 350

Phe Phe Ile Thr Asp Gln Gly Arg Ser Gly Lys Gln Pro Thr Gly Gln
355 360 365

Gln Gln Trp Gly Asp Trp Cys Asn Val Ile Gly Thr Gly Phe Gly Ile
370 375 380

Arg Pro Ser Ala Asn Thr Gly Asp Ser Leu Leu Asp Ser Phe Val Trp
385 390 395 400

Val Lys Pro Gly Gly Glu Cys Asp Gly Thr Ser Asp Ser Ser Ala Pro
405 410 415

Arg Phe Asp Ser His Cys Ala Leu Pro Asp Ala Leu Gln Pro Ala Pro
420 425 430

Gln Ala Gly Ala Trp Phe Gln Ala Tyr Phe Val Gln Leu Leu Thr Asn
435 440 445

Ala Asn Pro Ser Phe Leu
450

<210> 83
<211> 1317
<212> DNA
<213> Trichoderma reesei

60110USPCT1 Corrected SEQ LIST 2-2007.txt

<220>

<221> CDS

<222> (1)..(1317)

<223> Trichoderma reesei endoglucanase I

<400> 83

atg	cag	caa	ccg	gga	acc	agc	acc	ccc	gag	gtc	cat	ccc	aag	ttg	aca	48
Met	Gln	Gln	Pro	Gly	Thr	Ser	Thr	Pro	Glu	Val	His	Pro	Lys	Leu	Thr	
1				5					10					15		

acc	tac	aag	tgc	aca	aag	tcc	ggg	ggg	tgc	gtg	gcc	cag	gac	acc	tcg	96
Thr	Tyr	Lys	Cys	Thr	Lys	Ser	Gly	Gly	Cys	Val	Ala	Gln	Asp	Thr	Ser	
			20					25					30			

gtg	gtc	ctt	gac	tgg	aac	tac	cgc	tgg	atg	cac	gac	gca	aac	tac	aac	144
Val	Val	Leu	Asp	Trp	Asn	Tyr	Arg	Trp	Met	His	Asp	Ala	Asn	Tyr	Asn	
		35					40					45				

tcg	tgc	acc	gtc	aac	ggc	ggc	gtc	aac	acc	acg	ctc	tgc	cct	gac	gag	192
Ser	Cys	Thr	Val	Asn	Gly	Gly	Val	Asn	Thr	Thr	Leu	Cys	Pro	Asp	Glu	
	50					55					60					

gcg	acc	tgt	ggc	aag	aac	tgc	ttc	atc	gag	ggc	gtc	gac	tac	gcc	gcc	240
Ala	Thr	Cys	Gly	Lys	Asn	Cys	Phe	Ile	Glu	Gly	Val	Asp	Tyr	Ala	Ala	
65					70					75					80	

tcg	ggc	gtc	acg	acc	tcg	ggc	agc	agc	ctc	acc	atg	aac	cag	tac	atg	288
Ser	Gly	Val	Thr	Thr	Ser	Gly	Ser	Ser	Leu	Thr	Met	Asn	Gln	Tyr	Met	
				85					90					95		

ccc	agc	agc	tct	ggc	ggc	tac	agc	agc	gtc	tct	cct	cgg	ctg	tat	ctc	336
Pro	Ser	Ser	Ser	Gly	Gly	Tyr	Ser	Ser	Val	Ser	Pro	Arg	Leu	Tyr	Leu	
			100					105					110			

ctg	gac	tct	gac	ggt	gag	tac	gtg	atg	ctg	aag	ctc	aac	ggc	cag	gag	384
Leu	Asp	Ser	Asp	Gly	Glu	Tyr	Val	Met	Leu	Lys	Leu	Asn	Gly	Gln	Glu	
		115					120					125				

ctg	agc	ttc	gac	gtc	gac	ctc	tct	gct	ctg	ccg	tgt	gga	gag	aac	ggc	432
Leu	Ser	Phe	Asp	Val	Asp	Leu	Ser	Ala	Leu	Pro	Cys	Gly	Glu	Asn	Gly	
	130					135					140					

tcg	ctc	tac	ctg	tct	cag	atg	gac	gag	aac	ggg	ggc	gcc	aac	cag	tat	480
Ser	Leu	Tyr	Leu	Ser	Gln	Met	Asp	Glu	Asn	Gly	Gly	Ala	Asn	Gln	Tyr	
145					150					155					160	

aac	acg	gcc	ggt	gcc	aac	tac	ggg	agc	ggc	tac	tgc	gat	gct	cag	tgc	528
Asn	Thr	Ala	Gly	Ala	Asn	Tyr	Gly	Ser	Gly	Tyr	Cys	Asp	Ala	Gln	Cys	
				165					170					175		

ccc	gtc	cag	aca	tgg	agg	aac	ggc	acc	ctc	aac	act	agc	cac	cag	ggc	576
Pro	Val	Gln	Thr	Trp	Arg	Asn	Gly	Thr	Leu	Asn	Thr	Ser	His	Gln	Gly	
			180					185					190			

ttc	tgc	tgc	aac	gag	atg	gat	atc	ctg	gag	ggc	aac	tcg	agg	gcg	aat	624
Phe	Cys	Cys	Asn	Glu	Met	Asp	Ile	Leu	Glu	Gly	Asn	Ser	Arg	Ala	Asn	
		195					200					205				

gcc	ttg	acc	cct	cac	tct	tgc	acg	gcc	acg	gcc	tgc	gac	tct	gcc	ggt	672
Ala	Leu	Thr	Pro	His	Ser	Cys	Thr	Ala	Thr	Ala	Cys	Asp	Ser	Ala	Gly	
	210					215					220					

60110USPCT1 Corrected SEQ LIST 2-2007.txt

tgc ggc ttc aac ccc tat ggc agc ggc tac aaa agc tac tac ggc ccc Cys Gly Phe Asn Pro Tyr Gly Ser Gly Tyr Lys Ser Tyr Tyr Gly Pro 225 230 235 240	720
gga gat acc gtt gac acc tcc aag acc ttc acc atc atc acc cag ttc Gly Asp Thr Val Asp Thr Ser Lys Thr Phe Thr Ile Ile Thr Gln Phe 245 250 255	768
aac acg gac aac ggc tcg ccc tcg ggc aac ctt gtg agc atc acc cgc Asn Thr Asp Asn Gly Ser Pro Ser Gly Asn Leu Val Ser Ile Thr Arg 260 265 270	816
aag tac cag caa aac ggc gtc gac atc ccc agc gcc cag ccc ggc ggc Lys Tyr Gln Gln Asn Gly Val Asp Ile Pro Ser Ala Gln Pro Gly Gly 275 280 285	864
gac acc atc tcg tcc tgc ccg tcc gcc tca gcc tac ggc ggc ctc gcc Asp Thr Ile Ser Ser Cys Pro Ser Ala Ser Ala Tyr Gly Gly Leu Ala 290 295 300	912
acc atg ggc aag gcc ctg agc agc ggc atg gtg ctc gtg ttc agc att Thr Met Gly Lys Ala Leu Ser Ser Gly Met Val Leu Val Phe Ser Ile 305 310 315 320	960
tgg aac gac aac agc cag tac atg aac tgg ctc gac agc ggc aac gcc Trp Asn Asp Asn Ser Gln Tyr Met Asn Trp Leu Asp Ser Gly Asn Ala 325 330 335	1008
ggc ccc tgc agc agc acc gag ggc aac cca tcc aac acc ctg gcc aac Gly Pro Cys Ser Ser Thr Glu Gly Asn Pro Ser Asn Thr Leu Ala Asn 340 345 350	1056
aac ccc aac acg cac gtc gtc ttc tcc aac atc cgc tgg gga gac att Asn Pro Asn Thr His Val Val Phe Ser Asn Ile Arg Trp Gly Asp Ile 355 360 365	1104
ggg tct act acg aac tcg act gcg ccc ccg ccc ccg cct gcg tcc agc Gly Ser Thr Thr Asn Ser Thr Ala Pro Pro Pro Pro Ala Ser Ser 370 375 380	1152
acg acg ttt tcg act aca cgg agg agc tcg acg act tcg agc agc ccg Thr Thr Phe Ser Thr Thr Arg Arg Ser Ser Thr Thr Ser Ser Pro 385 390 395 400	1200
agc tgc acg cag act cac tgg ggg cag tgc ggt ggc att ggg tac agc Ser Cys Thr Gln Thr His Trp Gly Gln Cys Gly Gly Ile Gly Tyr Ser 405 410 415	1248
ggg tgc aag acg tgc acg tcg ggc act acg tgc cag tat agc aac gac Gly Cys Lys Thr Cys Thr Ser Gly Thr Thr Cys Gln Tyr Ser Asn Asp 420 425 430	1296
tac tac tcg caa tgc ctt tag Tyr Tyr Ser Gln Cys Leu 435	1317

<210> 84
 <211> 438
 <212> PRT
 <213> Trichoderma reesei

<400> 84

Met Gln Gln Pro Gly Thr Ser Thr Pro Glu Val His Pro Lys Leu Thr
 1 5 10 15

Thr Tyr Lys Cys Thr Lys Ser Gly Gly Cys Val Ala Gln Asp Thr Ser
 20 25 30

Val Val Leu Asp Trp Asn Tyr Arg Trp Met His Asp Ala Asn Tyr Asn
 35 40 45

Ser Cys Thr Val Asn Gly Gly Val Asn Thr Thr Leu Cys Pro Asp Glu
 50 55 60

Ala Thr Cys Gly Lys Asn Cys Phe Ile Glu Gly Val Asp Tyr Ala Ala
 65 70 75 80

Ser Gly Val Thr Thr Ser Gly Ser Ser Leu Thr Met Asn Gln Tyr Met
 85 90 95

Pro Ser Ser Ser Gly Gly Tyr Ser Ser Val Ser Pro Arg Leu Tyr Leu
 100 105 110

Leu Asp Ser Asp Gly Glu Tyr Val Met Leu Lys Leu Asn Gly Gln Glu
 115 120 125

Leu Ser Phe Asp Val Asp Leu Ser Ala Leu Pro Cys Gly Glu Asn Gly
 130 135 140

Ser Leu Tyr Leu Ser Gln Met Asp Glu Asn Gly Gly Ala Asn Gln Tyr
 145 150 155 160

Asn Thr Ala Gly Ala Asn Tyr Gly Ser Gly Tyr Cys Asp Ala Gln Cys
 165 170 175

Pro Val Gln Thr Trp Arg Asn Gly Thr Leu Asn Thr Ser His Gln Gly
 180 185 190

Phe Cys Cys Asn Glu Met Asp Ile Leu Glu Gly Asn Ser Arg Ala Asn
 195 200 205

Ala Leu Thr Pro His Ser Cys Thr Ala Thr Ala Cys Asp Ser Ala Gly
 210 215 220

Cys Gly Phe Asn Pro Tyr Gly Ser Gly Tyr Lys Ser Tyr Tyr Gly Pro
 225 230 235 240

Gly Asp Thr Val Asp Thr Ser Lys Thr Phe Thr Ile Ile Thr Gln Phe
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Asn Thr Asp Asn Gly Ser Pro Ser Gly Asn Leu Val Ser Ile Thr Arg
260 265 270

Lys Tyr Gln Gln Asn Gly Val Asp Ile Pro Ser Ala Gln Pro Gly Gly
275 280 285

Asp Thr Ile Ser Ser Cys Pro Ser Ala Ser Ala Tyr Gly Gly Leu Ala
290 295 300

Thr Met Gly Lys Ala Leu Ser Ser Gly Met Val Leu Val Phe Ser Ile
305 310 315 320

Trp Asn Asp Asn Ser Gln Tyr Met Asn Trp Leu Asp Ser Gly Asn Ala
325 330 335

Gly Pro Cys Ser Ser Thr Glu Gly Asn Pro Ser Asn Thr Leu Ala Asn
340 345 350

Asn Pro Asn Thr His Val Val Phe Ser Asn Ile Arg Trp Gly Asp Ile
355 360 365

Gly Ser Thr Thr Asn Ser Thr Ala Pro Pro Pro Pro Ala Ser Ser
370 375 380

Thr Thr Phe Ser Thr Thr Arg Arg Ser Ser Thr Thr Ser Ser Ser Pro
385 390 395 400

Ser Cys Thr Gln Thr His Trp Gly Gln Cys Gly Gly Ile Gly Tyr Ser
405 410 415

Gly Cys Lys Thr Cys Thr Ser Gly Thr Thr Cys Gln Tyr Ser Asn Asp
420 425 430

Tyr Tyr Ser Gln Cys Leu
435

<210> 85
<211> 954
<212> DNA
<213> Artificial Sequence

<220>
<223> 6GP1

<220>
<221> CDS
<222> (1)..(954)

60110USPCT1 Corrected SEQ LIST 2-2007.txt

<223> 6GP1

<400> 85

atg ggc gtg gac ccg ttc gag cgc aac aag atc ctc ggc cgc ggc atc Met Gly Val Asp Pro Phe Glu Arg Asn Lys Ile Leu Gly Arg Gly Ile 1 5 10 15	48
aac atc ggc aac gcc ctg gag gcc ccg aac gag ggc gac tgg ggc gtg Asn Ile Gly Asn Ala Leu Glu Ala Pro Asn Glu Gly Asp Trp Gly Val 20 25 30	96
gtg atc aag gac gag ttc ttc gac atc atc aag gag gcc ggc ttc tcc Val Ile Lys Asp Glu Phe Phe Asp Ile Ile Lys Glu Ala Gly Phe Ser 35 40 45	144
cac gtg cgc atc ccg atc cgc tgg tcc acc cac gcc tac gcc ttc ccg His Val Arg Ile Pro Ile Arg Trp Ser Thr His Ala Tyr Ala Phe Pro 50 55 60	192
ccg tac aag atc atg gac cgc ttc ttc aag cgc gtg gac gag gtg atc Pro Tyr Lys Ile Met Asp Arg Phe Phe Lys Arg Val Asp Glu Val Ile 65 70 75 80	240
aac ggc gcc ctc aag cgc ggc ctc gcc gtg gcc atc aac atc cac cac Asn Gly Ala Leu Lys Arg Gly Leu Ala Val Ala Ile Asn Ile His His 85 90 95	288
tac gag gag ctc atg aac gac ccg gag gag cac aag gag cgc ttc ctc Tyr Glu Glu Leu Met Asn Asp Pro Glu Glu His Lys Glu Arg Phe Leu 100 105 110	336
gcc ctc tgg aag cag atc gcc gac cgc tac aag gac tac ccg gag acc Ala Leu Trp Lys Gln Ile Ala Asp Arg Tyr Lys Asp Tyr Pro Glu Thr 115 120 125	384
ctc ttc ttc gag atc ctc aac gag ccg cac ggc aac ctc acc ccg gag Leu Phe Phe Glu Ile Leu Asn Glu Pro His Gly Asn Leu Thr Pro Glu 130 135 140	432
aag tgg aac gag ctg ctc gag gag gcc ctc aag gtg atc cgc tcc atc Lys Trp Asn Glu Leu Leu Glu Glu Ala Leu Lys Val Ile Arg Ser Ile 145 150 155 160	480
gac aag aag cac acc atc atc att ggc acc gca gag tgg gga ggc atc Asp Lys Lys His Thr Ile Ile Ile Gly Thr Ala Glu Trp Gly Gly Ile 165 170 175	528
tcc gcc ctc gag aag ctc tcc gtg ccg aag tgg gag aag aat tcc atc Ser Ala Leu Glu Lys Leu Ser Val Pro Lys Trp Glu Lys Asn Ser Ile 180 185 190	576
gtg acc atc cac tac tac aac ccg ttc gag ttc acg cac cag ggc gcc Val Thr Ile His Tyr Tyr Asn Pro Phe Glu Phe Thr His Gln Gly Ala 195 200 205	624
gag tgg gtg gag ggc tcc gag aag tgg ctt ggc cgc aag tgg ggc tcc Glu Trp Val Glu Gly Ser Glu Lys Trp Leu Gly Arg Lys Trp Gly Ser 210 215 220	672
ccg gac gac cag aag cac ctc atc gag gag ttc aac ttc atc gag gag Pro Asp Asp Gln Lys His Leu Ile Glu Glu Phe Asn Phe Ile Glu Glu 225 230 235 240	720

60110USPCT1 Corrected SEQ LIST 2-2007.txt

tgg tcc aag aag aac aag cgc ccg atc tac atc ggc gag ttt ggc gcc	768
Trp Ser Lys Lys Asn Lys Arg Pro Ile Tyr Ile Gly Glu Phe Gly Ala	
245 250 255	
tac cgc aag gcc gac ctc gag tcc cgc atc aag tgg acc tcc ttc gtg	816
Tyr Arg Lys Ala Asp Leu Glu Ser Arg Ile Lys Trp Thr Ser Phe Val	
260 265 270	
gtg cgt gag atg gag aag cgc cgc tgg tcc tgg gcc tac tgg gag ttc	864
Val Arg Glu Met Glu Lys Arg Arg Trp Ser Trp Ala Tyr Trp Glu Phe	
275 280 285	
tgc tcc ggc ttc ggc gtg tac gac acc ctc cgc aag acc tgg aac aag	912
Cys Ser Gly Phe Gly Val Tyr Asp Thr Leu Arg Lys Thr Trp Asn Lys	
290 295 300	
gac ctc ctc gag gcc ctc atc ggc ggc gac tcc atc gag tag	954
Asp Leu Leu Glu Ala Leu Ile Gly Gly Asp Ser Ile Glu	
305 310 315	

<210> 86
 <211> 317
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 86

Met Gly Val Asp Pro Phe Glu Arg Asn Lys Ile Leu Gly Arg Gly Ile
 1 5 10 15

Asn Ile Gly Asn Ala Leu Glu Ala Pro Asn Glu Gly Asp Trp Gly Val
 20 25 30

Val Ile Lys Asp Glu Phe Phe Asp Ile Ile Lys Glu Ala Gly Phe Ser
 35 40 45

His Val Arg Ile Pro Ile Arg Trp Ser Thr His Ala Tyr Ala Phe Pro
 50 55 60

Pro Tyr Lys Ile Met Asp Arg Phe Phe Lys Arg Val Asp Glu Val Ile
 65 70 75 80

Asn Gly Ala Leu Lys Arg Gly Leu Ala Val Ala Ile Asn Ile His His
 85 90 95

Tyr Glu Glu Leu Met Asn Asp Pro Glu Glu His Lys Glu Arg Phe Leu
 100 105 110

Ala Leu Trp Lys Gln Ile Ala Asp Arg Tyr Lys Asp Tyr Pro Glu Thr
 115 120 125

60110USPCT1 Corrected SEQ LIST 2-2007.txt

Leu Phe Phe Glu Ile Leu Asn Glu Pro His Gly Asn Leu Thr Pro Glu
130 135 140

Lys Trp Asn Glu Leu Leu Glu Glu Ala Leu Lys Val Ile Arg Ser Ile
145 150 155 160

Asp Lys Lys His Thr Ile Ile Ile Gly Thr Ala Glu Trp Gly Gly Ile
165 170 175

Ser Ala Leu Glu Lys Leu Ser Val Pro Lys Trp Glu Lys Asn Ser Ile
180 185 190

Val Thr Ile His Tyr Tyr Asn Pro Phe Glu Phe Thr His Gln Gly Ala
195 200 205

Glu Trp Val Glu Gly Ser Glu Lys Trp Leu Gly Arg Lys Trp Gly Ser
210 215 220

Pro Asp Asp Gln Lys His Leu Ile Glu Glu Phe Asn Phe Ile Glu Glu
225 230 235 240

Trp Ser Lys Lys Asn Lys Arg Pro Ile Tyr Ile Gly Glu Phe Gly Ala
245 250 255

Tyr Arg Lys Ala Asp Leu Glu Ser Arg Ile Lys Trp Thr Ser Phe Val
260 265 270

Val Arg Glu Met Glu Lys Arg Arg Trp Ser Trp Ala Tyr Trp Glu Phe
275 280 285

Cys Ser Gly Phe Gly Val Tyr Asp Thr Leu Arg Lys Thr Trp Asn Lys
290 295 300

Asp Leu Leu Glu Ala Leu Ile Gly Gly Asp Ser Ile Glu
305 310 315

<210> 87
<211> 1248
<212> DNA
<213> Hordeum vulgare

<220>
<221> CDS
<222> (1)..(1248)
<223> Barley AmyI amylase

<400> 87
atg gca cac caa gtc ctc ttt cag ggg ttc aac tgg gag tcg tgg aag
Met Ala His Gln Val Leu Phe Gln Gly Phe Asn Trp Glu Ser Trp Lys
1 5 10 15

60110USPCT1 Corrected SEQ LIST 2-2007.txt

cag	agc	ggc	ggg	tgg	tac	aac	atg	atg	atg	ggc	aag	gtc	gac	gac	atc	96
Gln	Ser	Gly	Gly	Trp	Tyr	Asn	Met	Met	Met	Gly	Lys	Val	Asp	Asp	Ile	
			20					25					30			
gcc	gct	gcc	gga	gtc	acc	cac	gtc	tgg	ctg	cca	ccg	ccg	tcg	cac	tcc	144
Ala	Ala	Ala	Gly	Val	Thr	His	Val	Trp	Leu	Pro	Pro	Pro	Ser	His	Ser	
			35				40					45				
gtc	tcc	aac	gaa	ggt	tac	atg	cct	ggt	cgg	ctg	tac	gac	atc	gac	gcg	192
Val	Ser	Asn	Glu	Gly	Tyr	Met	Pro	Gly	Arg	Leu	Tyr	Asp	Ile	Asp	Ala	
	50					55					60					
tcc	aag	tac	ggc	aac	gcg	gcg	gag	ctc	aag	tcg	ctc	atc	ggc	gcg	ctc	240
Ser	Lys	Tyr	Gly	Asn	Ala	Ala	Glu	Leu	Lys	Ser	Leu	Ile	Gly	Ala	Leu	
65					70					75					80	
cac	ggc	aag	ggc	gtg	cag	gcc	atc	gcc	gac	atc	gtc	atc	aac	cac	cgc	288
His	Gly	Lys	Gly	Val	Gln	Ala	Ile	Ala	Asp	Ile	Val	Ile	Asn	His	Arg	
				85					90					95		
tgc	gcc	gac	tac	aag	gat	agc	cg	ggc	atc	tac	tgc	atc	ttc	gag	ggc	336
Cys	Ala	Asp	Tyr	Lys	Asp	Ser	Arg	Gly	Ile	Tyr	Cys	Ile	Phe	Glu	Gly	
			100					105					110			
ggc	acc	tcc	gac	ggc	cg	ctc	gac	tgg	ggc	ccc	cac	atg	atc	tgt	cg	384
Gly	Thr	Ser	Asp	Gly	Arg	Leu	Asp	Trp	Gly	Pro	His	Met	Ile	Cys	Arg	
			115				120					125				
gac	gac	acc	aaa	tac	tcc	gat	ggc	acc	gca	aac	ctc	gac	acc	gga	gcc	432
Asp	Asp	Thr	Lys	Tyr	Ser	Asp	Gly	Thr	Ala	Asn	Leu	Asp	Thr	Gly	Ala	
			130			135					140					
gac	ttc	gcc	gcc	gcg	ccc	gac	atc	gac	cac	ctc	aac	gac	cg	gtc	cag	480
Asp	Phe	Ala	Ala	Ala	Pro	Asp	Ile	Asp	His	Leu	Asn	Asp	Arg	Val	Gln	
145					150					155					160	
cg	gag	ctc	aag	gag	tgg	ctc	ctc	tgg	ctc	aag	agc	gac	ctc	ggc	ttc	528
Arg	Glu	Leu	Lys	Glu	Trp	Leu	Leu	Trp	Leu	Lys	Ser	Asp	Leu	Gly	Phe	
				165				170						175		
gac	gcg	tgg	cg	ctt	gac	ttc	gcc	agg	ggc	tac	tcg	ccg	gag	atg	gcc	576
Asp	Ala	Trp	Arg	Leu	Asp	Phe	Ala	Arg	Gly	Tyr	Ser	Pro	Glu	Met	Ala	
			180					185					190			
aag	gtg	tac	atc	gac	ggc	aca	tcc	ccg	agc	ctc	gcc	gtg	gcc	gag	gtg	624
Lys	Val	Tyr	Ile	Asp	Gly	Thr	Ser	Pro	Ser	Leu	Ala	Val	Ala	Glu	Val	
			195				200					205				
tgg	gac	aat	atg	gcc	acc	ggc	ggc	gac	ggc	aag	ccc	aac	tac	gac	cag	672
Trp	Asp	Asn	Met	Ala	Thr	Gly	Gly	Asp	Gly	Lys	Pro	Asn	Tyr	Asp	Gln	
	210					215					220					
gac	gcg	cac	cg	cag	aat	ctg	gtg	aac	tgg	gtg	gac	aag	gtg	ggc	ggc	720
Asp	Ala	His	Arg	Gln	Asn	Leu	Val	Asn	Trp	Val	Asp	Lys	Val	Gly	Gly	
225					230					235					240	
gcg	gcc	tcg	gca	ggc	atg	gtg	ttc	gac	ttc	acg	acc	aaa	ggg	ata	ctg	768
Ala	Ala	Ser	Ala	Gly	Met	Val	Phe	Asp	Phe	Thr	Thr	Lys	Gly	Ile	Leu	
				245					250					255		
aac	gct	gcc	gtg	gag	ggc	gag	ctg	tgg	agg	ctg	atc	gac	ccg	cag	ggg	816
Asn	Ala	Ala	Val	Glu	Gly	Glu	Leu	Trp	Arg	Leu	Ile	Asp	Pro	Gln	Gly	

60110USPCT1 Corrected SEQ LIST 2-2007.txt

260	265	270	
aag gcc ccc ggc gtg atg gga tgg tgg ccg gcc aag gcc gtc acc ttc Lys Ala Pro Gly Val Met Gly Trp Trp Pro Ala Lys Ala Val Thr Phe 275 280 285			864
gtc gac aac cac gat aca ggc tcc acg cag gcc atg tgg cca ttc ccc Val Asp Asn His Asp Thr Gly Ser Thr Gln Ala Met Trp Pro Phe Pro 290 295 300			912
tcc gac aag gtc atg cag ggc tac gcg tac atc ctc acc cac ccc ggc Ser Asp Lys Val Met Gln Gly Tyr Ala Tyr Ile Leu Thr His Pro Gly 305 310 315 320			960
atc cca tgc atc ttc tac gac cat ttc ttc aac tgg ggg ttt aag gac Ile Pro Cys Ile Phe Tyr Asp His Phe Phe Asn Trp Gly Phe Lys Asp 325 330 335			1008
cag atc gcg gcg ctg gtg gcg atc agg aag cgc aac ggc atc acg gcg Gln Ile Ala Ala Leu Val Ala Ile Arg Lys Arg Asn Gly Ile Thr Ala 340 345 350			1056
acg agc gct ctg aag atc ctc atg cac gaa gga gat gcc tac gtc gcc Thr Ser Ala Leu Lys Ile Leu Met His Glu Gly Asp Ala Tyr Val Ala 355 360 365			1104
gag ata gac ggc aag gtg gtg gtg aag atc ggg tcc agg tac gac gtc Glu Ile Asp Gly Lys Val Val Val Lys Ile Gly Ser Arg Tyr Asp Val 370 375 380			1152
ggg gcg gtg atc ccg gcc ggc ttc gtg acc tcg gca cac ggc aac gac Gly Ala Val Ile Pro Ala Gly Phe Val Thr Ser Ala His Gly Asn Asp 385 390 395 400			1200
tac gcc gtc tgg gag aag aac ggt gcc gcg gca aca cta caa cgg agc Tyr Ala Val Trp Glu Lys Asn Gly Ala Ala Ala Thr Leu Gln Arg Ser 405 410 415			1248

<210> 88
 <211> 416
 <212> PRT
 <213> Hordeum vulgare

<400> 88

Met Ala His Gln Val Leu Phe Gln Gly Phe Asn Trp Glu Ser Trp Lys
 1 5 10 15

Gln Ser Gly Gly Trp Tyr Asn Met Met Met Gly Lys Val Asp Asp Ile
 20 25 30

Ala Ala Ala Gly Val Thr His Val Trp Leu Pro Pro Pro Ser His Ser
 35 40 45

Val Ser Asn Glu Gly Tyr Met Pro Gly Arg Leu Tyr Asp Ile Asp Ala
 50 55 60

Ser Lys Tyr Gly Asn Ala Ala Glu Leu Lys Ser Leu Ile Gly Ala Leu
 Page 88

65

His Gly Lys Gly Val Gln Ala Ile Ala Asp Ile Val Ile Asn His Arg
85 90 95

Cys Ala Asp Tyr Lys Asp Ser Arg Gly Ile Tyr Cys Ile Phe Glu Gly
100 105 110

Gly Thr Ser Asp Gly Arg Leu Asp Trp Gly Pro His Met Ile Cys Arg
115 120 125

Asp Asp Thr Lys Tyr Ser Asp Gly Thr Ala Asn Leu Asp Thr Gly Ala
130 135 140

Asp Phe Ala Ala Ala Pro Asp Ile Asp His Leu Asn Asp Arg Val Gln
145 150 155 160

Arg Glu Leu Lys Glu Trp Leu Leu Trp Leu Lys Ser Asp Leu Gly Phe
165 170 175

Asp Ala Trp Arg Leu Asp Phe Ala Arg Gly Tyr Ser Pro Glu Met Ala
180 185 190

Lys Val Tyr Ile Asp Gly Thr Ser Pro Ser Leu Ala Val Ala Glu Val
195 200 205

Trp Asp Asn Met Ala Thr Gly Gly Asp Gly Lys Pro Asn Tyr Asp Gln
210 215 220

Asp Ala His Arg Gln Asn Leu Val Asn Trp Val Asp Lys Val Gly Gly
225 230 235 240

Ala Ala Ser Ala Gly Met Val Phe Asp Phe Thr Thr Lys Gly Ile Leu
245 250 255

Asn Ala Ala Val Glu Gly Glu Leu Trp Arg Leu Ile Asp Pro Gln Gly
260 265 270

Lys Ala Pro Gly Val Met Gly Trp Trp Pro Ala Lys Ala Val Thr Phe
275 280 285

Val Asp Asn His Asp Thr Gly Ser Thr Gln Ala Met Trp Pro Phe Pro
290 295 300

Ser Asp Lys Val Met Gln Gly Tyr Ala Tyr Ile Leu Thr His Pro Gly
305 310 315 320

60110USPCT1 Corrected SEQ LIST 2-2007.txt

Ile Pro Cys Ile Phe Tyr Asp His Phe Phe Asn Trp Gly Phe Lys Asp
 325 330 335

Gln Ile Ala Ala Leu Val Ala Ile Arg Lys Arg Asn Gly Ile Thr Ala
 340 345 350

Thr Ser Ala Leu Lys Ile Leu Met His Glu Gly Asp Ala Tyr Val Ala
 355 360 365

Glu Ile Asp Gly Lys Val Val Val Lys Ile Gly Ser Arg Tyr Asp Val
 370 375 380

Gly Ala Val Ile Pro Ala Gly Phe Val Thr Ser Ala His Gly Asn Asp
 385 390 395 400

Tyr Ala Val Trp Glu Lys Asn Gly Ala Ala Ala Thr Leu Gln Arg Ser
 405 410 415

<210> 89

<211> 1401

<212> DNA

<213> Artificial Sequence

<220>

<223> Trichoderma reesei β -Glucosidase 2

<220>

<221> CDS

<222> (1)..(1401)

<223> Trichoderma reesei β -Glucosidase 2

<400> 89

atg ttg ccc aag gac ttt cag tgg ggg ttc gcc acg gct gcc tac cag 48
 Met Leu Pro Lys Asp Phe Gln Trp Gly Phe Ala Thr Ala Ala Tyr Gln
 1 5 10 15

atc gag ggc gcc gtc gac cag gac ggc cgc ggc ccc agc atc tgg gac 96
 Ile Glu Gly Ala Val Asp Gln Asp Gly Arg Gly Pro Ser Ile Trp Asp
 20 25 30

acg ttc tgc gcg cag ccc ggc aag atc gcc gac ggc tcg tcg ggc gtg 144
 Thr Phe Cys Ala Gln Pro Gly Lys Ile Ala Asp Gly Ser Ser Gly Val
 35 40 45

acg gcg tgc gac tcg tac aac cgc acg gcc gag gac att gcg ctg ctg 192
 Thr Ala Cys Asp Ser Tyr Asn Arg Thr Ala Glu Asp Ile Ala Leu Leu
 50 55 60

aag tcg ctc ggg gcc aag agc tac cgc ttc tcc atc tcg tgg tcg cgc 240
 Lys Ser Leu Gly Ala Lys Ser Tyr Arg Phe Ser Ile Ser Trp Ser Arg
 65 70 75 80

atc atc ccc gag ggc ggc cgc ggc gat gcc gtc aac cag gcg ggc atc 288
 Ile Ile Pro Glu Gly Gly Arg Gly Asp Ala Val Asn Gln Ala Gly Ile
 85 90 95

60110USPCT1 Corrected SEQ LIST 2-2007.txt

gac Asp	cac His	tac Tyr	gtc Val 100	aag Lys	ttc Phe	gtc Val	gac Asp 105	gac Asp 105	ctg Leu	ctc Leu	gac Asp	gcc Ala 110	ggc Gly 110	atc Ile	acg Thr	336
ccc Pro	ttc Phe	atc Ile 115	acc Thr	ctc Leu	ttc Phe	cac His	tgg Trp 120	gac Asp	ctg Leu	ccc Pro	gag Glu	ggc Gly 125	ctg Leu	cat His	cag Gln	384
cgg Arg	tac Tyr 130	ggg Gly	ggg Gly	ctg Leu	ctg Leu	aac Asn 135	cgc Arg	acc Thr	gag Glu	ttc Phe	ccg Pro 140	ctc Leu	gac Asp	ttt Phe	gaa Glu	432
aac Asn 145	tac Tyr	gcc Ala	cgc Arg	gtc Val 150	atg Met	ttc Phe	agg Arg	gcg Ala	ctg Leu	ccc Pro 155	aag Lys	gtg Val	cgc Arg	aac Asn	tgg Trp 160	480
atc Ile	acc Thr	ttc Phe	aac Asn	gag Glu 165	ccg Pro	ctg Leu	tgc Cys	tcg Ser	gcc Ala 170	atc Ile	ccg Pro	ggc Gly	tac Tyr	ggc Gly 175	tcc Ser	528
ggc Gly	acc Thr	ttc Phe	gcc Ala 180	ccc Pro	ggc Gly	cgg Arg	cag Gln	agc Ser 185	acc Thr	tcg Ser	gag Glu	ccg Pro	tgg Trp 190	acc Thr	gtc Val	576
ggc Gly	cac His	aac Asn 195	atc Ile	ctc Leu	gtc Val	gcc Ala	cac His 200	ggc Gly	cgc Arg	gcc Ala	gtc Val	aag Lys 205	gcg Ala	tac Tyr	cgc Arg	624
gac Asp 210	gac Asp	ttc Phe	aag Lys	ccc Pro	gcc Ala	agc Ser 215	ggc Gly	gac Asp	ggc Gly	cag Gln	atc Ile 220	ggc Gly	atc Ile	gtc Val	ctc Leu	672
aac Asn 225	ggc Gly	gac Asp	ttc Phe	acc Thr	tac Tyr 230	ccc Pro	tgg Trp	gac Asp	gcc Ala	gcc Ala 235	gac Asp	ccg Pro	gcc Ala	gac Asp	aag Lys 240	720
gag Glu	gcg Ala	gcc Ala	gag Glu	cgg Arg 245	cgc Arg	ctc Leu	gag Glu	ttc Phe	ttc Phe 250	acg Thr	gcc Ala	tgg Trp	ttc Phe	gcg Ala 255	gac Asp	768
ccc Pro	atc Ile	tac Tyr	ttg Leu 260	ggc Gly	gac Asp	tac Tyr	ccg Pro	gcg Ala 265	tcg Ser	atg Met	cgc Arg	aag Lys	cag Gln 270	ctg Leu	ggc Gly	816
gac Asp	cgg Arg 275	ctg Leu	ccg Pro	acc Thr	ttt Phe	acg Thr	ccc Pro 280	gag Glu	gag Glu	cgc Arg	gcc Ala	ctc Leu 285	gtc Val	cac His	ggc Gly	864
tcc Ser	aac Asn 290	gac Asp	ttt Phe	tac Tyr	ggc Gly	atg Met 295	aac Asn	cac His	tac Tyr	acg Thr	tcc Ser 300	aac Asn	tac Tyr	atc Ile	cgc Arg	912
cac His 305	cgc Arg	agc Ser	tcg Ser	ccc Pro	gcc Ala 310	tcc Ser	gcc Ala	gac Asp	gac Asp	acc Thr 315	gtc Val	ggc Gly	aac Asn	gtc Val	gac Asp 320	960
gtg Val	ctc Leu	ttc Phe	acc Thr	aac Asn 325	aag Lys	cag Gln	ggc Gly	aac Asn	tgc Cys 330	atc Ile	ggc Gly	ccc Pro	gag Glu	acg Thr 335	cag Gln	1008
tcc Ser	ccc Pro	tgg Trp	ctg Leu 340	cgc Arg	ccc Pro	tgt Cys	gcc Ala	gcc Ala 345	ggc Gly	ttc Phe	cgc Arg	gac Asp	ttc Phe 350	ctg Leu	gtg Val	1056

60110USPCT1 Corrected SEQ LIST 2-2007.txt

tgg atc agc aag agg tac ggc tac ccg ccc atc tac gtg acg gag aac Trp Ile Ser Lys Arg Tyr Gly Tyr Pro Pro Ile Tyr Val Thr Glu Asn 355 360 365	1104
ggc acg agc atc aag ggc gag agc gac ttg ccc aag gag aag att ctc Gly Thr Ser Ile Lys Gly Glu Ser Asp Leu Pro Lys Glu Lys Ile Leu 370 375 380	1152
gaa gat gac ttc agg gtc aag tac tat aac gag tac atc cgt gcc atg Glu Asp Asp Phe Arg Val Lys Tyr Tyr Asn Glu Tyr Ile Arg Ala Met 385 390 395 400	1200
gtt acc gcc gtg gag ctg gac ggg gtc aac gtc aag ggg tac ttt gcc Val Thr Ala Val Glu Leu Asp Gly Val Asn Val Lys Gly Tyr Phe Ala 405 410 415	1248
tgg tcg ctc atg gac aac ttt gag tgg gcg gac ggc tac gtg acg agg Trp Ser Leu Met Asp Asn Phe Glu Trp Ala Asp Gly Tyr Val Thr Arg 420 425 430	1296
ttt ggg gtt acg tat gtg gat tat gag aat ggg cag aag cgg ttc ccc Phe Gly Val Thr Tyr Val Asp Tyr Glu Asn Gly Gln Lys Arg Phe Pro 435 440 445	1344
aag aag agc gca aag agc ttg aag ccg ctg ttt gac gag ctg att gcg Lys Lys Ser Ala Lys Ser Leu Lys Pro Leu Phe Asp Glu Leu Ile Ala 450 455 460	1392
gcg gcg tga Ala Ala 465	1401

<210> 90
 <211> 466
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 90

Met	Leu	Pro	Lys	Asp	Phe	Gln	Trp	Gly	Phe	Ala	Thr	Ala	Ala	Tyr	Gln
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Ile	Glu	Gly	Ala	Val	Asp	Gln	Asp	Gly	Arg	Gly	Pro	Ser	Ile	Trp	Asp
			20					25					30		
Thr	Phe	Cys	Ala	Gln	Pro	Gly	Lys	Ile	Ala	Asp	Gly	Ser	Ser	Gly	Val
		35					40					45			
Thr	Ala	Cys	Asp	Ser	Tyr	Asn	Arg	Thr	Ala	Glu	Asp	Ile	Ala	Leu	Leu
	50					55					60				
Lys	Ser	Leu	Gly	Ala	Lys	Ser	Tyr	Arg	Phe	Ser	Ile	Ser	Trp	Ser	Arg
65					70				75						80

60110USPCT1 Corrected SEQ LIST 2-2007.txt

Ile Ile Pro Glu Gly Gly Arg Gly Asp Ala Val Asn Gln Ala Gly Ile
85 90 95

Asp His Tyr Val Lys Phe Val Asp Asp Leu Leu Asp Ala Gly Ile Thr
100 105 110

Pro Phe Ile Thr Leu Phe His Trp Asp Leu Pro Glu Gly Leu His Gln
115 120 125

Arg Tyr Gly Gly Leu Leu Asn Arg Thr Glu Phe Pro Leu Asp Phe Glu
130 135 140

Asn Tyr Ala Arg Val Met Phe Arg Ala Leu Pro Lys Val Arg Asn Trp
145 150 155 160

Ile Thr Phe Asn Glu Pro Leu Cys Ser Ala Ile Pro Gly Tyr Gly Ser
165 170 175

Gly Thr Phe Ala Pro Gly Arg Gln Ser Thr Ser Glu Pro Trp Thr Val
180 185 190

Gly His Asn Ile Leu Val Ala His Gly Arg Ala Val Lys Ala Tyr Arg
195 200 205

Asp Asp Phe Lys Pro Ala Ser Gly Asp Gly Gln Ile Gly Ile Val Leu
210 215 220

Asn Gly Asp Phe Thr Tyr Pro Trp Asp Ala Ala Asp Pro Ala Asp Lys
225 230 235 240

Glu Ala Ala Glu Arg Arg Leu Glu Phe Phe Thr Ala Trp Phe Ala Asp
245 250 255

Pro Ile Tyr Leu Gly Asp Tyr Pro Ala Ser Met Arg Lys Gln Leu Gly
260 265 270

Asp Arg Leu Pro Thr Phe Thr Pro Glu Glu Arg Ala Leu Val His Gly
275 280 285

Ser Asn Asp Phe Tyr Gly Met Asn His Tyr Thr Ser Asn Tyr Ile Arg
290 295 300

His Arg Ser Ser Pro Ala Ser Ala Asp Asp Thr Val Gly Asn Val Asp
305 310 315 320

Val Leu Phe Thr Asn Lys Gln Gly Asn Cys Ile Gly Pro Glu Thr Gln
325 330 335

60110USPCT1 Corrected SEQ LIST 2-2007.txt

Ser Pro Trp Leu Arg Pro Cys Ala Ala Gly Phe Arg Asp Phe Leu Val
340 345 350

Trp Ile Ser Lys Arg Tyr Gly Tyr Pro Pro Ile Tyr Val Thr Glu Asn
355 360 365

Gly Thr Ser Ile Lys Gly Glu Ser Asp Leu Pro Lys Glu Lys Ile Leu
370 375 380

Glu Asp Asp Phe Arg Val Lys Tyr Tyr Asn Glu Tyr Ile Arg Ala Met
385 390 395 400

Val Thr Ala Val Glu Leu Asp Gly Val Asn Val Lys Gly Tyr Phe Ala
405 410 415

Trp Ser Leu Met Asp Asn Phe Glu Trp Ala Asp Gly Tyr Val Thr Arg
420 425 430

Phe Gly Val Thr Tyr Val Asp Tyr Glu Asn Gly Gln Lys Arg Phe Pro
435 440 445

Lys Lys Ser Ala Lys Ser Leu Lys Pro Leu Phe Asp Glu Leu Ile Ala
450 455 460

Ala Ala
465

<210> 91
<211> 2103
<212> DNA
<213> Artificial Sequence

<220>
<223> Trichoderma reesei β -Glucosidase D

<220>
<221> CDS
<222> (1)..(2103)
<223> Trichoderma reesei β -Glucosidase D

<400> 91
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1 5 10 15

ttt gtc gcc aac gac cag gag cac gag cgg cga gcg gtc gac tgt ctc 96
Phe Val Ala Asn Asp Gln Glu His Glu Arg Arg Ala Val Asp Cys Leu
20 25 30

atc acc cag cgg gct ctc cgg gag gtc tat ctg cga ccc ttc cag atc 144
Ile Thr Gln Arg Ala Leu Arg Glu Val Tyr Leu Arg Pro Phe Gln Ile
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60110USPCT1 Corrected SEQ LIST 2-2007.txt

35	40	45	
gta gcc cga gat gca agg ccc ggc gca ttg atg aca tcc tac aac aag Val Ala Arg Asp Ala Arg Pro Gly Ala Leu Met Thr Ser Tyr Asn Lys 50 55 60			192
gtc aat ggc aag cac gtc gct gac agc gcc gag ttc ctt cag ggc att Val Asn Gly Lys His Val Ala Asp Ser Ala Glu Phe Leu Gln Gly Ile 65 70 75 80			240
ctc cgg act gag tgg aat tgg gac cct ctc att gtc agc gac tgg tac Leu Arg Thr Glu Trp Asn Trp Asp Pro Leu Ile Val Ser Asp Trp Tyr 85 90 95			288
ggc acc tac acc act att gat gcc atc aaa gcc ggc ctt gat ctc gag Gly Thr Tyr Thr Thr Ile Asp Ala Ile Lys Ala Gly Leu Asp Leu Glu 100 105 110			336
atg ccg ggc gtt tca cga tat cgc ggc aaa tac atc gag tct gct ctg Met Pro Gly Val Ser Arg Tyr Arg Gly Lys Tyr Ile Glu Ser Ala Leu 115 120 125			384
cag gcc cgt ttg ctg aag cag tcc act atc gat gag cgc gct cgc cgc Gln Ala Arg Leu Leu Lys Gln Ser Thr Ile Asp Glu Arg Ala Arg Arg 130 135 140			432
gtg ctc agg ttc gcc cag aag gcc agc cat ctc aag gtc tcc gag gta Val Leu Arg Phe Ala Gln Lys Ala Ser His Leu Lys Val Ser Glu Val 145 150 155 160			480
gag caa ggc cgt gac ttc cca gag gat cgc gtc ctc aac cgt cag atc Glu Gln Gly Arg Asp Phe Pro Glu Asp Arg Val Leu Asn Arg Gln Ile 165 170 175			528
tgc ggc agc agc att gtc cta ctg aag aat gag aac tcc atc tta cct Cys Gly Ser Ser Ile Val Leu Leu Lys Asn Glu Asn Ser Ile Leu Pro 180 185 190			576
ctc ccc aag tcc gtc aag aag gtc gcc ctt gtt ggt tcc cac gtg cgt Leu Pro Lys Ser Val Lys Lys Val Ala Leu Val Gly Ser His Val Arg 195 200 205			624
cta ccg gct atc tcg gga gga ggc agc gcc tct ctt gtc cct tac tat Leu Pro Ala Ile Ser Gly Gly Ser Ala Ser Leu Val Pro Tyr Tyr 210 215 220			672
gcc ata tct cta tac gat gcc gtc tct gag gta cta gcc ggt gcc acg Ala Ile Ser Leu Tyr Asp Ala Val Ser Glu Val Leu Ala Gly Ala Thr 225 230 235 240			720
atc acg cac gag gtc ggt gcc tat gcc cac caa atg ctg ccc gtc atc Ile Thr His Glu Val Gly Ala Tyr Ala His Gln Met Leu Pro Val Ile 245 250 255			768
gac gca atg atc agc aac gcc gta atc cac ttc tac aac gac ccc atc Asp Ala Met Ile Ser Asn Ala Val Ile His Phe Tyr Asn Asp Pro Ile 260 265 270			816
gat gtc aaa gac aga aag ctc ctt ggc agt gag aac gta tcg tcg aca Asp Val Lys Asp Arg Lys Leu Leu Gly Ser Glu Asn Val Ser Ser Thr 275 280 285			864
tcg ttc cag ctc atg gat tac aac aac atc cca acg ctc aac aag gcc			912

60110USPCT1 Corrected SEQ LIST 2-2007.txt

Ser	Phe	Gln	Leu	Met	Asp	Tyr	Asn	Asn	Ile	Pro	Thr	Leu	Asn	Lys	Ala	
290						295					300					
atg	ttc	tgg	ggt	act	ctc	gtg	ggc	gag	ttt	atc	cct	acc	gcc	acg	gga	960
Met	Phe	Trp	Gly	Thr	Leu	Val	Gly	Glu	Phe	Ile	Pro	Thr	Ala	Thr	Gly	
305					310				315						320	
att	tgg	gaa	ttt	ggc	ctc	agt	gtc	ttt	ggc	act	gcc	gac	ctt	tat	att	1008
Ile	Trp	Glu	Phe	Gly	Leu	Ser	Val	Phe	Gly	Thr	Ala	Asp	Leu	Tyr	Ile	
				325					330					335		
gat	aat	gag	ctc	gtg	att	gaa	aat	aca	aca	cat	cag	acg	cgt	gga	acc	1056
Asp	Asn	Glu	Leu	Val	Ile	Glu	Asn	Thr	Thr	His	Gln	Thr	Arg	Gly	Thr	
			340					345					350			
gcc	ttt	ttc	gga	aag	gga	acg	acg	gaa	aaa	gtc	gct	acc	agg	agg	atg	1104
Ala	Phe	Phe	Gly	Lys	Gly	Thr	Thr	Glu	Lys	Val	Ala	Thr	Arg	Arg	Met	
		355					360					365				
gtg	gcc	ggc	agc	acc	tac	aag	ctg	cgt	ctc	gag	ttt	ggg	tct	gcc	aac	1152
Val	Ala	Gly	Ser	Thr	Tyr	Lys	Leu	Arg	Leu	Glu	Phe	Gly	Ser	Ala	Asn	
	370					375					380					
acg	acc	aag	atg	gag	acg	acc	ggt	gtt	gtc	aac	ttt	ggc	ggc	ggt	gcc	1200
Thr	Thr	Lys	Met	Glu	Thr	Thr	Gly	Val	Val	Asn	Phe	Gly	Gly	Gly	Ala	
385					390					395					400	
gta	cac	ctg	ggt	gcc	tgt	ctc	aag	gtc	gac	cca	cag	gag	atg	att	gcg	1248
Val	His	Leu	Gly	Ala	Cys	Leu	Lys	Val	Asp	Pro	Gln	Glu	Met	Ile	Ala	
				405					410					415		
cgg	gcc	gtc	aag	gcc	gca	gcc	gat	gcc	gac	tac	acc	atc	atc	tgc	acg	1296
Arg	Ala	Val	Lys	Ala	Ala	Ala	Asp	Ala	Asp	Tyr	Thr	Ile	Ile	Cys	Thr	
			420					425					430			
gga	ctc	agc	ggc	gag	tgg	gag	tct	gag	ggt	ttt	gac	cgg	cct	cac	atg	1344
Gly	Leu	Ser	Gly	Glu	Trp	Glu	Ser	Glu	Gly	Phe	Asp	Arg	Pro	His	Met	
		435					440					445				
gac	ctg	ccc	cct	ggt	gtg	gac	acc	atg	atc	tcg	caa	gtt	ctt	gac	gcc	1392
Asp	Leu	Pro	Pro	Gly	Val	Asp	Thr	Met	Ile	Ser	Gln	Val	Leu	Asp	Ala	
	450					455					460					
gct	ccc	aat	gct	gta	gtc	gtc	aac	cag	tca	ggc	acc	cca	gtg	aca	atg	1440
Ala	Pro	Asn	Ala	Val	Val	Val	Asn	Gln	Ser	Gly	Thr	Pro	Val	Thr	Met	
465				470						475					480	
agc	tgg	gct	cat	aaa	gca	aag	gcc	att	gtg	cag	gct	tgg	tat	ggt	ggt	1488
Ser	Trp	Ala	His	Lys	Ala	Lys	Ala	Ile	Val	Gln	Ala	Trp	Tyr	Gly	Gly	
				485					490					495		
aac	gag	aca	ggc	cac	gga	atc	tcc	gat	gtg	ctc	ttt	ggc	aac	gtc	aac	1536
Asn	Glu	Thr	Gly	His	Gly	Ile	Ser	Asp	Val	Leu	Phe	Gly	Asn	Val	Asn	
			500					505					510			
ccg	tcg	ggg	aaa	ctc	tcc	cta	tcg	tgg	cca	gtc	gat	gtg	aag	cac	aac	1584
Pro	Ser	Gly	Lys	Leu	Ser	Leu	Ser	Trp	Pro	Val	Asp	Val	Lys	His	Asn	
		515					520					525				
cca	gca	tat	ctc	aac	tac	gcc	agc	gtt	ggt	gga	cgg	gtc	ttg	tat	ggc	1632
Pro	Ala	Tyr	Leu	Asn	Tyr	Ala	Ser	Val	Gly	Gly	Arg	Val	Leu	Tyr	Gly	
	530					535					540					

60110USPCT1 Corrected SEQ LIST 2-2007.txt

gag gat gtt tac gtt ggc tac aag ttc tac gac aaa acg gag agg gag Glu Asp Val Tyr Val Gly Tyr Lys Phe Tyr Asp Lys Thr Glu Arg Glu 545 550 555 560	1680
gtt ctg ttt cct ttt ggg cat ggc ctg tct tac gct acc ttc aag ctc Val Leu Phe Pro Phe Gly His Gly Leu Ser Tyr Ala Thr Phe Lys Leu 565 570 575	1728
cca gat tct acc gtg agg acg gtc ccc gaa acc ttc cac ccg gac cag Pro Asp Ser Thr Val Arg Thr Val Pro Glu Thr Phe His Pro Asp Gln 580 585 590	1776
ccc aca gta gcc att gtc aag atc aag aac acg agc agt gtc ccg ggc Pro Thr Val Ala Ile Val Lys Ile Lys Asn Thr Ser Ser Val Pro Gly 595 600 605	1824
gcc cag gtc ctg cag tta tac att tcg gcc cca aac tcg cct aca cat Ala Gln Val Leu Gln Leu Tyr Ile Ser Ala Pro Asn Ser Pro Thr His 610 615 620	1872
cgc ccg gtc aag gag ctg cac gga ttc gaa aag gtg tat ctt gaa gct Arg Pro Val Lys Glu Leu His Gly Phe Glu Lys Val Tyr Leu Glu Ala 625 630 635 640	1920
ggc gag gag aag gag gta caa ata ccc att gac cag tac gct act agc Gly Glu Glu Lys Glu Val Gln Ile Pro Ile Asp Gln Tyr Ala Thr Ser 645 650 655	1968
ttc tgg gac gag att gag agc atg tgg aag agc gag agg ggc att tat Phe Trp Asp Glu Ile Glu Ser Met Trp Lys Ser Glu Arg Gly Ile Tyr 660 665 670	2016
gat gtg ctt gta gga ttc tcg agt cag gaa atc tcg ggc aag ggg aag Asp Val Leu Val Gly Phe Ser Ser Gln Glu Ile Ser Gly Lys Gly Lys 675 680 685	2064
ctg att gtg cct gaa acg cga ttc tgg atg ggg ctg tag Leu Ile Val Pro Glu Thr Arg Phe Trp Met Gly Leu 690 695 700	2103

<210> 92
 <211> 700
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 92

Met Ile Leu Gly Cys Glu Ser Thr Gly Val Ile Ser Ala Val Lys His
 1 5 10 15

Phe Val Ala Asn Asp Gln Glu His Glu Arg Arg Ala Val Asp Cys Leu
 20 25 30

Ile Thr Gln Arg Ala Leu Arg Glu Val Tyr Leu Arg Pro Phe Gln Ile
 35 40 45

60110USPCT1 Corrected SEQ LIST 2-2007.txt

Val Ala Arg Asp Ala Arg Pro Gly Ala Leu Met Thr Ser Tyr Asn Lys
 50 55 60
 Val Asn Gly Lys His Val Ala Asp Ser Ala Glu Phe Leu Gln Gly Ile
 65 70 75 80
 Leu Arg Thr Glu Trp Asn Trp Asp Pro Leu Ile Val Ser Asp Trp Tyr
 85 90 95
 Gly Thr Tyr Thr Thr Ile Asp Ala Ile Lys Ala Gly Leu Asp Leu Glu
 100 105 110
 Met Pro Gly Val Ser Arg Tyr Arg Gly Lys Tyr Ile Glu Ser Ala Leu
 115 120 125
 Gln Ala Arg Leu Leu Lys Gln Ser Thr Ile Asp Glu Arg Ala Arg Arg
 130 135 140
 Val Leu Arg Phe Ala Gln Lys Ala Ser His Leu Lys Val Ser Glu Val
 145 150 155 160
 Glu Gln Gly Arg Asp Phe Pro Glu Asp Arg Val Leu Asn Arg Gln Ile
 165 170 175
 Cys Gly Ser Ser Ile Val Leu Leu Lys Asn Glu Asn Ser Ile Leu Pro
 180 185 190
 Leu Pro Lys Ser Val Lys Lys Val Ala Leu Val Gly Ser His Val Arg
 195 200 205
 Leu Pro Ala Ile Ser Gly Gly Gly Ser Ala Ser Leu Val Pro Tyr Tyr
 210 215 220
 Ala Ile Ser Leu Tyr Asp Ala Val Ser Glu Val Leu Ala Gly Ala Thr
 225 230 235 240
 Ile Thr His Glu Val Gly Ala Tyr Ala His Gln Met Leu Pro Val Ile
 245 250 255
 Asp Ala Met Ile Ser Asn Ala Val Ile His Phe Tyr Asn Asp Pro Ile
 260 265 270
 Asp Val Lys Asp Arg Lys Leu Leu Gly Ser Glu Asn Val Ser Ser Thr
 275 280 285
 Ser Phe Gln Leu Met Asp Tyr Asn Asn Ile Pro Thr Leu Asn Lys Ala
 290 295 300

60110USPCT1 Corrected SEQ LIST 2-2007.txt

Met Phe Trp Gly Thr Leu Val Gly Glu Phe Ile Pro Thr Ala Thr Gly
305 310 315 320

Ile Trp Glu Phe Gly Leu Ser Val Phe Gly Thr Ala Asp Leu Tyr Ile
325 330 335

Asp Asn Glu Leu Val Ile Glu Asn Thr Thr His Gln Thr Arg Gly Thr
340 345 350

Ala Phe Phe Gly Lys Gly Thr Thr Glu Lys Val Ala Thr Arg Arg Met
355 360 365

Val Ala Gly Ser Thr Tyr Lys Leu Arg Leu Glu Phe Gly Ser Ala Asn
370 375 380

Thr Thr Lys Met Glu Thr Thr Gly Val Val Asn Phe Gly Gly Gly Ala
385 390 395 400

Val His Leu Gly Ala Cys Leu Lys Val Asp Pro Gln Glu Met Ile Ala
405 410 415

Arg Ala Val Lys Ala Ala Ala Asp Ala Asp Tyr Thr Ile Ile Cys Thr
420 425 430

Gly Leu Ser Gly Glu Trp Glu Ser Glu Gly Phe Asp Arg Pro His Met
435 440 445

Asp Leu Pro Pro Gly Val Asp Thr Met Ile Ser Gln Val Leu Asp Ala
450 455 460

Ala Pro Asn Ala Val Val Val Asn Gln Ser Gly Thr Pro Val Thr Met
465 470 475 480

Ser Trp Ala His Lys Ala Lys Ala Ile Val Gln Ala Trp Tyr Gly Gly
485 490 495

Asn Glu Thr Gly His Gly Ile Ser Asp Val Leu Phe Gly Asn Val Asn
500 505 510

Pro Ser Gly Lys Leu Ser Leu Ser Trp Pro Val Asp Val Lys His Asn
515 520 525

Pro Ala Tyr Leu Asn Tyr Ala Ser Val Gly Gly Arg Val Leu Tyr Gly
530 535 540

Glu Asp Val Tyr Val Gly Tyr Lys Phe Tyr Asp Lys Thr Glu Arg Glu
545 550 555 560

60110USPCT1 Corrected SEQ LIST 2-2007.txt

Val Leu Phe Pro Phe Gly His Gly Leu Ser Tyr Ala Thr Phe Lys Leu
565 570 575

Pro Asp Ser Thr Val Arg Thr Val Pro Glu Thr Phe His Pro Asp Gln
580 585 590

Pro Thr Val Ala Ile Val Lys Ile Lys Asn Thr Ser Ser Val Pro Gly
595 600 605

Ala Gln Val Leu Gln Leu Tyr Ile Ser Ala Pro Asn Ser Pro Thr His
610 615 620

Arg Pro Val Lys Glu Leu His Gly Phe Glu Lys Val Tyr Leu Glu Ala
625 630 635 640

Gly Glu Glu Lys Glu Val Gln Ile Pro Ile Asp Gln Tyr Ala Thr Ser
645 650 655

Phe Trp Asp Glu Ile Glu Ser Met Trp Lys Ser Glu Arg Gly Ile Tyr
660 665 670

Asp Val Leu Val Gly Phe Ser Ser Gln Glu Ile Ser Gly Lys Gly Lys
675 680 685

Leu Ile Val Pro Glu Thr Arg Phe Trp Met Gly Leu
690 695 700

<210> 93
<211> 1496
<212> DNA
<213> Artificial Sequence

<220>
<223> Maize optimized CBHI

<400> 93
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60110USPCT1 Corrected SEQ LIST 2-2007.txt

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 <223> Maize optimized CBHII

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<211> 1317

<212> DNA

<213> Artificial Sequence

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<223> Maize optimized EGLI

<400> 95

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<212> DNA

<213> Artificial Sequence

<220>

<223> Maize optimized BGLII

<400> 96

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gacaacttcg agtgggccga cggctacgtg acccgcttcg gcgtgaccta cgtggactac	1320
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 <211> 2103
 <212> DNA
 <213> Artificial Sequence

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 <223> Maize optimized CEL3D

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 <212> DNA
 <213> Zea mays

<220>
 <223> Q protein promoter

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<210> 99
 <211> 1188
 <212> DNA
 <213> artificial sequence

<220>

<223> synthetic ferulic acid esterase

<400> 99

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<210> 100

<211> 395

<212> PRT

<213> artificial sequence

<220>

<223> synthetic ferulic acid esterase

<400> 100

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Thr Ala Thr Asn Ser Thr Arg Pro Ala Arg Val Tyr Leu Pro Pro Gly

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35

Tyr Ser Lys Asp Lys Lys Tyr Ser Val Leu Tyr Leu Leu His Gly Ile
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Gly Gly Ser Glu Asn Asp Trp Phe Glu Gly Gly Gly Arg Ala Asn Val
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Ile Ala Asp Asn Leu Ile Ala Glu Gly Lys Ile Lys Pro Leu Ile Ile
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Val Thr Pro Asn Thr Asn Ala Ala Gly Pro Gly Ile Ala Asp Gly Tyr
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Glu Asn Phe Thr Lys Asp Leu Leu Asn Ser Leu Ile Pro Tyr Ile Glu
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Ser Asn Tyr Ser Val Tyr Thr Asp Arg Glu His Arg Ala Ile Ala Gly
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Leu Ser Met Gly Gly Gly Gln Ser Phe Asn Ile Gly Leu Thr Asn Leu
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Asp Lys Phe Ala Tyr Ile Gly Pro Ile Ser Ala Ala Pro Asn Thr Tyr
 165 170 175

Pro Asn Glu Arg Leu Phe Pro Asp Gly Gly Lys Ala Ala Arg Glu Lys
 180 185 190

Leu Lys Leu Leu Phe Ile Ala Cys Gly Thr Asn Asp Ser Leu Ile Gly
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Phe Gly Gln Arg Val His Glu Tyr Cys Val Ala Asn Asn Ile Asn His
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Val Tyr Trp Leu Ile Gln Gly Gly Gly His Asp Phe Asn Val Trp Lys
 225 230 235 240

Pro Gly Leu Trp Asn Phe Leu Gln Met Ala Asp Glu Ala Gly Leu Thr
 245 250 255

Arg Asp Gly Asn Thr Pro Val Pro Thr Pro Ser Pro Lys Pro Ala Asn
 260 265 270

Thr Arg Ile Glu Ala Glu Asp Tyr Asp Gly Ile Asn Ser Ser Ser Ile
 275 280 285

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Glu Ile Ile Gly Val Pro Pro Glu Gly Gly Arg Gly Ile Gly Tyr Ile
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Thr Ser Gly Asp Tyr Leu Val Tyr Lys Ser Ile Asp Phe Gly Asn Gly
305 310 315 320

Ala Thr Ser Phe Lys Ala Lys Val Ala Asn Ala Asn Thr Ser Asn Ile
325 330 335

Glu Leu Arg Leu Asn Gly Pro Asn Gly Thr Leu Ile Gly Thr Leu Ser
340 345 350

Val Lys Ser Thr Gly Asp Trp Asn Thr Tyr Glu Glu Gln Thr Cys Ser
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Ile Ser Lys Val Thr Gly Ile Asn Asp Leu Tyr Leu Val Phe Lys Gly
370 375 380

Pro Val Asn Ile Asp Trp Phe Thr Phe Gly Val
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<211> 1188
<212> DNA
<213> artificial sequence

<220>
<223> plasmid 13036

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<210> 102
<211> 395
<212> PRT
<213> artificial sequence

<220>
<223> plasmid 13036

<400> 102

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Thr Ala Thr Asn Ser Thr Arg Pro Ala Arg Val Tyr Leu Pro Pro Gly
35 40 45

Tyr Ser Lys Asp Lys Lys Tyr Ser Val Leu Tyr Leu Leu His Gly Ile
50 55 60

Gly Gly Ser Glu Asn Asp Trp Phe Glu Gly Gly Gly Arg Ala Asn Val
65 70 75 80

Ile Ala Asp Asn Leu Ile Ala Glu Gly Lys Ile Lys Pro Leu Ile Ile
85 90 95

Val Thr Pro Asn Thr Asn Ala Ala Gly Pro Gly Ile Ala Asp Gly Tyr
100 105 110

Glu Asn Phe Thr Lys Asp Leu Leu Asn Ser Leu Ile Pro Tyr Ile Glu
115 120 125

Ser Asn Tyr Ser Val Tyr Thr Asp Arg Glu His Arg Ala Ile Ala Gly
130 135 140

Leu Ser Met Gly Gly Gly Gln Ser Phe Asn Ile Gly Leu Thr Asn Leu
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60110USPCT1 Corrected SEQ LIST 2-2007.txt

Asp Lys Phe Ala Tyr Ile Gly Pro Ile Ser Ala Ala Pro Asn Thr Tyr
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Pro Asn Glu Arg Leu Phe Pro Asp Gly Gly Lys Ala Ala Arg Glu Lys
180 185 190

Leu Lys Leu Leu Phe Ile Ala Cys Gly Thr Asn Asp Ser Leu Ile Gly
195 200 205

Phe Gly Gln Arg Val His Glu Tyr Cys Val Ala Asn Asn Ile Asn His
210 215 220

Val Tyr Trp Leu Ile Gln Gly Gly Gly His Asp Phe Asn Val Trp Lys
225 230 235 240

Pro Gly Leu Trp Asn Phe Leu Gln Met Ala Asp Glu Ala Gly Leu Thr
245 250 255

Arg Asp Gly Asn Thr Pro Val Pro Thr Pro Ser Pro Lys Pro Ala Asn
260 265 270

Thr Arg Ile Glu Ala Glu Asp Tyr Asp Gly Ile Asn Ser Ser Ser Ile
275 280 285

Glu Ile Ile Gly Val Pro Pro Glu Gly Gly Arg Gly Ile Gly Tyr Ile
290 295 300

Thr Ser Gly Asp Tyr Leu Val Tyr Lys Ser Ile Asp Phe Gly Asn Gly
305 310 315 320

Ala Thr Ser Phe Lys Ala Lys Val Ala Asn Ala Asn Thr Ser Asn Ile
325 330 335

Glu Leu Arg Leu Asn Gly Pro Asn Gly Thr Leu Ile Gly Thr Leu Ser
340 345 350

Val Lys Ser Thr Gly Asp Trp Asn Thr Tyr Glu Glu Gln Thr Cys Ser
355 360 365

Ile Ser Lys Val Thr Gly Ile Asn Asp Leu Tyr Leu Val Phe Lys Gly
370 375 380

Pro Val Asn Ile Asp Trp Phe Thr Phe Gly Val
385 390 395

<210> 103

60110USPCT1 Corrected SEQ LIST 2-2007.txt

<211> 1245
 <212> DNA
 <213> artificial sequence

<220>
 <223> plasmid 13038

<400> 103
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 gccgcctccc tcccgaccat gccgccgtcc ggctacgacc aggtgcgcaa cggcgtgccg 120
 cgcggccagg tggatgaacat ctctacttc tccaccgcca ccaactccac ccgcccggcc 180
 cgcgtgtacc tcccgcgggg ctactccaag gacaagaagt actccgtgct ctacctctc 240
 caccggcatcg gcggctccga gaacgactgg ttcgagggcg gcggccgcgc caacgtgatc 300
 gccgacaacc tcatcgccga gggcaagatc aagccgctca tcatcgtgac cccgaacacc 360
 aacgccggcg gcccgggcat cgccgacggc tacgagaact tcaccaagga cctcctcaac 420
 tccctcatcc cgtacatcga gtccaactac tccgtgtaca ccgaccgcga gcaccgcgcc 480
 atcgccggcc tctctatggg cggcggccag tccttcaaca tcggcctcac caacctcgac 540
 aagttcgcct acatcgggcc gatctccgcc gcccgaaca cctaccgaa cgagcgcctc 600
 ttcccggacg gcggcaaggc cgcccgcgag aagctcaagc tcctcttcat cgctgcggc 660
 accaacgact cctcatcgg cttcggccag cgcgtgcacg agtactgcgt ggccaacaac 720
 atcaaccacg tgtactggct catccagggc ggcggccacg acttcaacgt gtggaagccg 780
 ggcctctgga acttctcca gatggccgac gaggccggcc tcaccgcga cggcaacacc 840
 ccggtgccga ccccgctccc gaagccggcc aacacccgca tcgaggccga ggactacgac 900
 ggcacaaact cctcctccat cgagatcatc ggcgtgccgc cggagggcgg ccgcggcatc 960
 ggctacatca cctccggcga ctacctcgtg tacaagtcca tcgacttcgg caacggcgcc 1020
 acctccttca aggccaaggt ggccaacgcc aacacctcca acatcgagct tcgcctcaac 1080
 ggcccgaacg gcaccctcat cggcaccctc tccgtgaagt ccaccggcga ctggaacacc 1140
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 ttcaagggcc cggatgaacat cgactgggtc accttcggcg ttag 1245

<210> 104
 <211> 414
 <212> PRT
 <213> artificial sequence

<220>
 <223> plasmid 13038 aa

<400> 104

Met Arg Val Leu Leu Val Ala Leu Ala Leu Leu Ala Leu Ala Ala Ser
 1 5 10 15

60110USPCT1 Corrected SEQ LIST 2-2007.txt

Ala Thr Ser Met Ala Ala Ser Leu Pro Thr Met Pro Pro Ser Gly Tyr
20 25 30

Asp Gln Val Arg Asn Gly Val Pro Arg Gly Gln Val Val Asn Ile Ser
35 40 45

Tyr Phe Ser Thr Ala Thr Asn Ser Thr Arg Pro Ala Arg Val Tyr Leu
50 55 60

Pro Pro Gly Tyr Ser Lys Asp Lys Lys Tyr Ser Val Leu Tyr Leu Leu
65 70 75 80

His Gly Ile Gly Gly Ser Glu Asn Asp Trp Phe Glu Gly Gly Gly Arg
85 90 95

Ala Asn Val Ile Ala Asp Asn Leu Ile Ala Glu Gly Lys Ile Lys Pro
100 105 110

Leu Ile Ile Val Thr Pro Asn Thr Asn Ala Ala Gly Pro Gly Ile Ala
115 120 125

Asp Gly Tyr Glu Asn Phe Thr Lys Asp Leu Leu Asn Ser Leu Ile Pro
130 135 140

Tyr Ile Glu Ser Asn Tyr Ser Val Tyr Thr Asp Arg Glu His Arg Ala
145 150 155 160

Ile Ala Gly Leu Ser Met Gly Gly Gly Gln Ser Phe Asn Ile Gly Leu
165 170 175

Thr Asn Leu Asp Lys Phe Ala Tyr Ile Gly Pro Ile Ser Ala Ala Pro
180 185 190

Asn Thr Tyr Pro Asn Glu Arg Leu Phe Pro Asp Gly Gly Lys Ala Ala
195 200 205

Arg Glu Lys Leu Lys Leu Leu Phe Ile Ala Cys Gly Thr Asn Asp Ser
210 215 220

Leu Ile Gly Phe Gly Gln Arg Val His Glu Tyr Cys Val Ala Asn Asn
225 230 235 240

Ile Asn His Val Tyr Trp Leu Ile Gln Gly Gly Gly His Asp Phe Asn
245 250 255

Val Trp Lys Pro Gly Leu Trp Asn Phe Leu Gln Met Ala Asp Glu Ala

260

265

270

Gly Leu Thr Arg Asp Gly Asn Thr Pro Val Pro Thr Pro Ser Pro Lys
 275 280 285

Pro Ala Asn Thr Arg Ile Glu Ala Glu Asp Tyr Asp Gly Ile Asn Ser
 290 295 300

Ser Ser Ile Glu Ile Ile Gly Val Pro Pro Glu Gly Gly Arg Gly Ile
 305 310 315 320

Gly Tyr Ile Thr Ser Gly Asp Tyr Leu Val Tyr Lys Ser Ile Asp Phe
 325 330 335

Gly Asn Gly Ala Thr Ser Phe Lys Ala Lys Val Ala Asn Ala Asn Thr
 340 345 350

Ser Asn Ile Glu Leu Arg Leu Asn Gly Pro Asn Gly Thr Leu Ile Gly
 355 360 365

Thr Leu Ser Val Lys Ser Thr Gly Asp Trp Asn Thr Tyr Glu Glu Gln
 370 375 380

Thr Cys Ser Ile Ser Lys Val Thr Gly Ile Asn Asp Leu Tyr Leu Val
 385 390 395 400

Phe Lys Gly Pro Val Asn Ile Asp Trp Phe Thr Phe Gly Val
 405 410

<210> 105
 <211> 1425
 <212> DNA
 <213> artificial sequence

<220>
 <223> plasmid 13039

<400> 105
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 gacgcgtcca cgttcgcgcg cggcgccgcg cagggcctga ggggggcccc ggcgtcggcg 120
 gcggcggaaca cgctcagcat gcggaccagc gcgcgcgcgg cggccaggca ccagcaccag 180
 caggcgcgcc gcggggccag gttcccgtcg ctcgtcgtgt gcgccagcgc cggcgccatg 240
 gccgcctccc tcccgaccat gccgccgtcc ggctacgacc aggtgcgcaa cggcgtgccg 300
 cgcggccagg tggtgaacat ctctacttc tccaccgcca ccaactccac ccgcccggcc 360
 cgcgtgtacc tcccgcggg ctactccaag gacaagaagt actccgtgct ctacctctc 420
 cacggcatcg gcggctccga gaacgactgg ttcgagggcg gcggccgcgc caacgtgatc 480

60110USPCT1 Corrected SEQ LIST 2-2007.txt

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aacgccgccc gcccgggcat cgccgacggc tacgagaact tcaccaagga cctcctcaac 600
tccctcatcc cgtacatcga gtccaactac tccgtgtaca ccgaccgcca gcaccgcgcc 660
atcgccggcc tctctatggg cggcggccag tccttcaaca tcggcctcac caacctcgac 720
aagttcgcct acatcggccc gatctccgcc gccccgaaca cctacccgaa cgagcgcctc 780
ttcccggacg gcggcaaggc cgcccgcgag aagctcaagc tcctcttcat cgcctgcggc 840
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atcaaccacg tgtactggct catccagggc ggcggccacg acttcaacgt gtggaagccg 960
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ccggtgccga ccccgcccc gaagccggcc aacaccgcca tcgaggcca ggactacgac 1080
ggcatcaact cctcctccat cgagatcatc ggcgtgccgc cggagggcgg ccgcggcatc 1140
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acctccttca aggccaaggt ggccaacgcc aacacctcca acatcgagct tcgcctcaac 1260
ggcccgaacg gcacctcat cggcaccctc tccgtgaagt ccaccggcca ctggaacacc 1320
tacgaggagc agacctgctc catctccaag gtgaccggca tcaacgacct ctacctcgtg 1380
ttcaagggcc cggtgaacat cgactgggtc accttcggcg tgtag 1425

<210> 106
<211> 474
<212> PRT
<213> artificial sequence

<220>
<223> plasmid 13039 aa

<400> 106

Met Leu Ala Ala Leu Ala Thr Ser Gln Leu Val Ala Thr Arg Ala Gly
1 5 10 15

Leu Gly Val Pro Asp Ala Ser Thr Phe Arg Arg Gly Ala Ala Gln Gly
20 25 30

Leu Arg Gly Ala Arg Ala Ser Ala Ala Ala Asp Thr Leu Ser Met Arg
35 40 45

Thr Ser Ala Arg Ala Ala Pro Arg His Gln His Gln Gln Ala Arg Arg
50 55 60

Gly Ala Arg Phe Pro Ser Leu Val Val Cys Ala Ser Ala Gly Ala Met
65 70 75 80

60110USPCT1 Corrected SEQ LIST 2-2007.txt

Ala Ala Ser Leu Pro Thr Met Pro Pro Ser Gly Tyr Asp Gln Val Arg
85 90 95

Asn Gly Val Pro Arg Gly Gln Val Val Asn Ile Ser Tyr Phe Ser Thr
100 105 110

Ala Thr Asn Ser Thr Arg Pro Ala Arg Val Tyr Leu Pro Pro Gly Tyr
115 120 125

Ser Lys Asp Lys Lys Tyr Ser Val Leu Tyr Leu Leu His Gly Ile Gly
130 135 140

Gly Ser Glu Asn Asp Trp Phe Glu Gly Gly Gly Arg Ala Asn Val Ile
145 150 155 160

Ala Asp Asn Leu Ile Ala Glu Gly Lys Ile Lys Pro Leu Ile Ile Val
165 170 175

Thr Pro Asn Thr Asn Ala Ala Gly Pro Gly Ile Ala Asp Gly Tyr Glu
180 185 190

Asn Phe Thr Lys Asp Leu Leu Asn Ser Leu Ile Pro Tyr Ile Glu Ser
195 200 205

Asn Tyr Ser Val Tyr Thr Asp Arg Glu His Arg Ala Ile Ala Gly Leu
210 215 220

Ser Met Gly Gly Gly Gln Ser Phe Asn Ile Gly Leu Thr Asn Leu Asp
225 230 235 240

Lys Phe Ala Tyr Ile Gly Pro Ile Ser Ala Ala Pro Asn Thr Tyr Pro
245 250 255

Asn Glu Arg Leu Phe Pro Asp Gly Gly Lys Ala Ala Arg Glu Lys Leu
260 265 270

Lys Leu Leu Phe Ile Ala Cys Gly Thr Asn Asp Ser Leu Ile Gly Phe
275 280 285

Gly Gln Arg Val His Glu Tyr Cys Val Ala Asn Asn Ile Asn His Val
290 295 300

Tyr Trp Leu Ile Gln Gly Gly Gly His Asp Phe Asn Val Trp Lys Pro
305 310 315 320

Gly Leu Trp Asn Phe Leu Gln Met Ala Asp Glu Ala Gly Leu Thr Arg
325 330 335

60110USPCT1 Corrected SEQ LIST 2-2007.txt

Asp Gly Asn Thr Pro Val Pro Thr Pro Ser Pro Lys Pro Ala Asn Thr
340 345 350

Arg Ile Glu Ala Glu Asp Tyr Asp Gly Ile Asn Ser Ser Ser Ile Glu
355 360 365

Ile Ile Gly Val Pro Pro Glu Gly Gly Arg Gly Ile Gly Tyr Ile Thr
370 375 380

Ser Gly Asp Tyr Leu Val Tyr Lys Ser Ile Asp Phe Gly Asn Gly Ala
385 390 395 400

Thr Ser Phe Lys Ala Lys Val Ala Asn Ala Asn Thr Ser Asn Ile Glu
405 410 415

Leu Arg Leu Asn Gly Pro Asn Gly Thr Leu Ile Gly Thr Leu Ser Val
420 425 430

Lys Ser Thr Gly Asp Trp Asn Thr Tyr Glu Glu Gln Thr Cys Ser Ile
435 440 445

Ser Lys Val Thr Gly Ile Asn Asp Leu Tyr Leu Val Phe Lys Gly Pro
450 455 460

Val Asn Ile Asp Trp Phe Thr Phe Gly Val
465 470

<210> 107
<211> 1263
<212> DNA
<213> artificial sequence

<220>
<223> plasmid 13347

<400> 107
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gccgcctccc tcccgaccat gccgccgtcc ggctacgacc aggtgcgcaa cggcgtgccg 120
cgcgggccagg tggatgaacat ctctacttcc tccaccgcca ccaactccac ccgcccggcc 180
cgcgtgtacc tcccgccggg ctactccaag gacaagaagt actccgtgct ctacctcctc 240
cacggcatcg gcgggtccga gaacgactgg ttcgagggcg gcggccgcgc caacgtgatc 300
gccgacaacc tcacgcccga gggcaagatc aagccgctca tcacgtgac cccgaacacc 360
aacgccgccg gcccgggcat cgccgacggc tacgagaact tcaccaagga cctcctcaac 420
tccctcatcc cgtacatcga gtccaactac tccgtgtaca ccgaccgcga gcaccgcgcc 480

60110USPCT1 Corrected SEQ LIST 2-2007.txt

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 aagttcgctt acatcgcccc gatctccgcc gccccgaaca cctacccgaa cgagcgcttc 600
 ttcccggacg gcggcaaggc cgcccgcgag aagctcaagc tcctcttcat cgcttgcggc 660
 accaacgact ccctcatcgg cttcggccag cgcgtgcacg agtactgcgt ggccaacaac 720
 atcaaccacg tgtactggct catccagggc ggcggccacg acttcaacgt gtggaagccg 780
 ggcctctgga acttcctcca gatggccgac gaggccggcc tcacccgcga cggcaacacc 840
 ccggtgccga ccccgctccc gaagccggcc aacacccgca tcgaggccga ggactacgac 900
 ggcatcaact cctcctccat cgagatcatc ggcgtgccgc cggagggcgg ccgcggcatc 960
 ggctacatca cctccggcga ctacctcgtg tacaagtcca tcgacttcgg caacggcgcc 1020
 acctccttca aggccaaggt ggccaacgcc aacacctcca acatcgagct tcgcctcaac 1080
 ggcgggaacg gcacccctcat cggcaccctc tccgtgaagt ccaccggcga ctggaacacc 1140
 tacgaggagc agacctgctc catctccaag gtgaccggca tcaacgacct ctacctcgtg 1200
 ttcaagggcc cgggtgaacat cgactggttc accttcggcg tgtccgagaa ggacgaactc 1260
 tag 1263

<210> 108
 <211> 420
 <212> PRT
 <213> artificial sequence

<220>
 <223> plasmid 13347

<400> 108

Met Arg Val Leu Leu Val Ala Leu Ala Leu Leu Ala Leu Ala Ala Ser
1 5 10 15

Ala Thr Ser Met Ala Ala Ser Leu Pro Thr Met Pro Pro Ser Gly Tyr
20 25 30

Asp Gln Val Arg Asn Gly Val Pro Arg Gly Gln Val Val Asn Ile Ser
35 40 45

Tyr Phe Ser Thr Ala Thr Asn Ser Thr Arg Pro Ala Arg Val Tyr Leu
50 55 60

Pro Pro Gly Tyr Ser Lys Asp Lys Lys Tyr Ser Val Leu Tyr Leu Leu
65 70 75 80

His Gly Ile Gly Gly Ser Glu Asn Asp Trp Phe Glu Gly Gly Gly Arg
85 90 95

60110USPCT1 Corrected SEQ LIST 2-2007.txt

Ala Asn Val Ile Ala Asp Asn Leu Ile Ala Glu Gly Lys Ile Lys Pro
 100 105 110

Leu Ile Ile Val Thr Pro Asn Thr Asn Ala Ala Gly Pro Gly Ile Ala
 115 120 125

Asp Gly Tyr Glu Asn Phe Thr Lys Asp Leu Leu Asn Ser Leu Ile Pro
 130 135 140

Tyr Ile Glu Ser Asn Tyr Ser Val Tyr Thr Asp Arg Glu His Arg Ala
 145 150 155 160

Ile Ala Gly Leu Ser Met Gly Gly Gly Gln Ser Phe Asn Ile Gly Leu
 165 170 175

Thr Asn Leu Asp Lys Phe Ala Tyr Ile Gly Pro Ile Ser Ala Ala Pro
 180 185 190

Asn Thr Tyr Pro Asn Glu Arg Leu Phe Pro Asp Gly Gly Lys Ala Ala
 195 200 205

Arg Glu Lys Leu Lys Leu Leu Phe Ile Ala Cys Gly Thr Asn Asp Ser
 210 215 220

Leu Ile Gly Phe Gly Gln Arg Val His Glu Tyr Cys Val Ala Asn Asn
 225 230 235 240

Ile Asn His Val Tyr Trp Leu Ile Gln Gly Gly Gly His Asp Phe Asn
 245 250 255

Val Trp Lys Pro Gly Leu Trp Asn Phe Leu Gln Met Ala Asp Glu Ala
 260 265 270

Gly Leu Thr Arg Asp Gly Asn Thr Pro Val Pro Thr Pro Ser Pro Lys
 275 280 285

Pro Ala Asn Thr Arg Ile Glu Ala Glu Asp Tyr Asp Gly Ile Asn Ser
 290 295 300

Ser Ser Ile Glu Ile Ile Gly Val Pro Pro Glu Gly Gly Arg Gly Ile
 305 310 315 320

Gly Tyr Ile Thr Ser Gly Asp Tyr Leu Val Tyr Lys Ser Ile Asp Phe
 325 330 335

Gly Asn Gly Ala Thr Ser Phe Lys Ala Lys Val Ala Asn Ala Asn Thr
 340 345 350

60110USPCT1 Corrected SEQ LIST 2-2007.txt

Ser Asn Ile Glu Leu Arg Leu Asn Gly Pro Asn Gly Thr Leu Ile Gly
355 360 365

Thr Leu Ser Val Lys Ser Thr Gly Asp Trp Asn Thr Tyr Glu Glu Gln
370 375 380

Thr Cys Ser Ile Ser Lys Val Thr Gly Ile Asn Asp Leu Tyr Leu Val
385 390 395 400

Phe Lys Gly Pro Val Asn Ile Asp Trp Phe Thr Phe Gly Val Ser Glu
405 410 415

Lys Asp Glu Leu
420

<210> 109
<211> 1296
<212> DNA
<213> artificial sequence

<220>
<223> plasmid 11267

<400> 109
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gcgcagtcgc agccggagct gaagctggag tccgtggtga tcgtgtcccg ccacggcgctg 120
cgcgccccga ccaaggccac ccagctcatg caggacgtga ccccgagcgc ctggccgacc 180
tggccggtga agctcggcga gctgaccccg cgcgccggcg agctgatcgc ctacctcggc 240
cactactggc gccagcgcct cgtggccgac ggctcctcc cgaagtgcgg ctgcccgcag 300
tccggccagg tggccatcat cgccgacgtg gacgagcgca cccgcaagac cggcgaggcc 360
ttcgccgccg gcctcgcccc ggactgcgcc atcaccgtgc acaccaggc cgacacctcc 420
tccccggacc cgctcttcaa cccgtcaag accggcgtgt gccagctcga caacgccaac 480
gtgaccgacg ccattctgga gcgcgccggc ggctccatcg ccgacttcac cggccactac 540
cagaccgcct tccgcgagct ggagcgcgtg ctcaacttcc cgcagtccaa cctctgcctc 600
aagcgcgaga agcaggacga gtcctgctcc ctcaccagg ccctcccgtc cgagctgaag 660
gtgtccgccc actgcgtgtc cctaccggc gccgtgtccc tcgcctccat gtcaccgaa 720
atcttctctc tccagcaggc ccagggcatg ccggagccgg gctggggccc catcaccgac 780
tcccaccagt ggaacacct cctctccctc cacaacgccc agttcgacct cctccagcgc 840
accccgagg tggcccgctc ccgcgccacc ccgtcctcg acctcatcaa gaccgccctc 900
accccgacc cgccgcagaa gcaggcctac ggcgtagacc tcccgacctc cgtgctcttc 960
atcgccggcc acgacaccaa cctcgccaac ctcgccggcg ccctggagct gaactggacc 1020

60110USPCT1 Corrected SEQ LIST 2-2007.txt

ctccccgggcc agccgggacaa caccgcccg ggcggcgagc tgggtgttcga gcgctggcgc 1080
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 atgcgcgaca agaccccgct ctccctcaac accccgccgg gcgaggtgaa gctcaccctc 1200
 gccggctgcg aggagcgcaa cgcccagggc atgtgctccc tcgccggctt caccagatc 1260
 gtgaacgagg cccgcatccc ggcctgctcc ctctaa 1296

<210> 110
 <211> 431
 <212> PRT
 <213> artificial sequence

<220>
 <223> plasmid 11267 aa sequence

<400> 110

Met Arg Val Leu Leu Val Ala Leu Ala Leu Leu Ala Leu Ala Ala Ser
 1 5 10 15

Ala Thr Ser Ala Ala Gln Ser Glu Pro Glu Leu Lys Leu Glu Ser Val
 20 25 30

Val Ile Val Ser Arg His Gly Val Arg Ala Pro Thr Lys Ala Thr Gln
 35 40 45

Leu Met Gln Asp Val Thr Pro Asp Ala Trp Pro Thr Trp Pro Val Lys
 50 55 60

Leu Gly Glu Leu Thr Pro Arg Gly Gly Glu Leu Ile Ala Tyr Leu Gly
 65 70 75 80

His Tyr Trp Arg Gln Arg Leu Val Ala Asp Gly Leu Leu Pro Lys Cys
 85 90 95

Gly Cys Pro Gln Ser Gly Gln Val Ala Ile Ile Ala Asp Val Asp Glu
 100 105 110

Arg Thr Arg Lys Thr Gly Glu Ala Phe Ala Ala Gly Leu Ala Pro Asp
 115 120 125

Cys Ala Ile Thr Val His Thr Gln Ala Asp Thr Ser Ser Pro Asp Pro
 130 135 140

Leu Phe Asn Pro Leu Lys Thr Gly Val Cys Gln Leu Asp Asn Ala Asn
 145 150 155 160

Val Thr Asp Ala Ile Leu Glu Arg Ala Gly Gly Ser Ile Ala Asp Phe
 Page 120

Thr Gly His Tyr Gln Thr Ala Phe Arg Glu Leu Glu Arg Val Leu Asn
180 185 190

Phe Pro Gln Ser Asn Leu Cys Leu Lys Arg Glu Lys Gln Asp Glu Ser
195 200 205

Cys Ser Leu Thr Gln Ala Leu Pro Ser Glu Leu Lys Val Ser Ala Asp
210 215 220

Cys Val Ser Leu Thr Gly Ala Val Ser Leu Ala Ser Met Leu Thr Glu
225 230 235 240

Ile Phe Leu Leu Gln Gln Ala Gln Gly Met Pro Glu Pro Gly Trp Gly
245 250 255

Arg Ile Thr Asp Ser His Gln Trp Asn Thr Leu Leu Ser Leu His Asn
260 265 270

Ala Gln Phe Asp Leu Leu Gln Arg Thr Pro Glu Val Ala Arg Ser Arg
275 280 285

Ala Thr Pro Leu Leu Asp Leu Ile Lys Thr Ala Leu Thr Pro His Pro
290 295 300

Pro Gln Lys Gln Ala Tyr Gly Val Thr Leu Pro Thr Ser Val Leu Phe
305 310 315 320

Ile Ala Gly His Asp Thr Asn Leu Ala Asn Leu Gly Gly Ala Leu Glu
325 330 335

Leu Asn Trp Thr Leu Pro Gly Gln Pro Asp Asn Thr Pro Pro Gly Gly
340 345 350

Glu Leu Val Phe Glu Arg Trp Arg Arg Leu Ser Asp Asn Ser Gln Trp
355 360 365

Ile Gln Val Ser Leu Val Phe Gln Thr Leu Gln Gln Met Arg Asp Lys
370 375 380

Thr Pro Leu Ser Leu Asn Thr Pro Pro Gly Glu Val Lys Leu Thr Leu
385 390 395 400

Ala Gly Cys Glu Glu Arg Asn Ala Gln Gly Met Cys Ser Leu Ala Gly
405 410 415

60110USPCT1 Corrected SEQ LIST 2-2007.txt

Phe Thr Gln Ile Val Asn Glu Ala Arg Ile Pro Ala Cys Ser Leu
 420 425 430

<210> 111
 <211> 1314
 <212> DNA
 <213> artificial sequence

<220>
 <223> plasmid 11268

<400> 111
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 cgcgccccga ccaaggccac ccagctcatg caggacgtga ccccgagcgc ctggccgacc 180
 tggccggtga agctcggcga gctgaccccg cgcggcggcg agctgatcgc ctacctcggc 240
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 tccggccagg tggccatcat cgccgacgtg gacgagcgca cccgcaagac cggcgaggcc 360
 ttcgcccgcg gcctcgcgcc ggactgcgcc atcaccgtgc acaccaggc cgacacctcc 420
 tccccggacc cgctcttcaa cccgctcaag accggcgtgt gccagctcga caacgccaac 480
 gtgaccgacg ccattcctga gcgcgccggc ggctccatcg ccgacttcac cggccactac 540
 cagaccgcct tccgcgagct ggagcgcgtg ctcaacttcc cgcagtccaa cctctgcctc 600
 aagcgcgaga agcaggacga gtcctgctcc ctacccagg ccctcccgtc cgagctgaag 660
 gtgtccgccc actgcgtgtc cctcaccggc gccgtgtccc tcgcctccat gtcaccgaa 720
 atcttctctc tccagcaggc ccagggcatg ccggagccgg gctggggccg catcaccgac 780
 tcccaccagt ggaacaccct cctctccctc cacaacgccc agttcgacct cctccagcgc 840
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 accccgcacc cgccgcagaa gcaggcctac ggcgtgacct tcccgacctc cgtgctcttc 960
 atcgccggcc acgacaccaa cctcgccaac ctcggcggcg ccctggagct gaactggacc 1020
 ctcccggggc agccggacaa caccgcggc ggcggcgagc tgggtgttcga gcgctggcgc 1080
 cgcctctccg acaactccca gtggattcag gtgtccctcg tgttcagac cctccagcag 1140
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 gccggctgcg aggagcgcga cgcggggc atgtgctccc tcgcccggctt caccagatc 1260
 gtgaacgagg cccgcatccc ggcctgctcc ctctccgaga aggacgagct gtaa 1314

<210> 112
 <211> 437
 <212> PRT
 <213> artificial sequence

60110USPCT1 Corrected SEQ LIST 2-2007.txt

<220>

<223> plasmid 11268 amino acid sequence

<400> 112

Met Arg Val Leu Leu Val Ala Leu Ala Leu Leu Ala Leu Ala Ala Ser
 1 5 10 15

Ala Thr Ser Ala Ala Gln Ser Glu Pro Glu Leu Lys Leu Glu Ser Val
 20 25 30

Val Ile Val Ser Arg His Gly Val Arg Ala Pro Thr Lys Ala Thr Gln
 35 40 45

Leu Met Gln Asp Val Thr Pro Asp Ala Trp Pro Thr Trp Pro Val Lys
 50 55 60

Leu Gly Glu Leu Thr Pro Arg Gly Gly Glu Leu Ile Ala Tyr Leu Gly
 65 70 75 80

His Tyr Trp Arg Gln Arg Leu Val Ala Asp Gly Leu Leu Pro Lys Cys
 85 90 95

Gly Cys Pro Gln Ser Gly Gln Val Ala Ile Ile Ala Asp Val Asp Glu
 100 105 110

Arg Thr Arg Lys Thr Gly Glu Ala Phe Ala Ala Gly Leu Ala Pro Asp
 115 120 125

Cys Ala Ile Thr Val His Thr Gln Ala Asp Thr Ser Ser Pro Asp Pro
 130 135 140

Leu Phe Asn Pro Leu Lys Thr Gly Val Cys Gln Leu Asp Asn Ala Asn
 145 150 155 160

Val Thr Asp Ala Ile Leu Glu Arg Ala Gly Gly Ser Ile Ala Asp Phe
 165 170 175

Thr Gly His Tyr Gln Thr Ala Phe Arg Glu Leu Glu Arg Val Leu Asn
 180 185 190

Phe Pro Gln Ser Asn Leu Cys Leu Lys Arg Glu Lys Gln Asp Glu Ser
 195 200 205

Cys Ser Leu Thr Gln Ala Leu Pro Ser Glu Leu Lys Val Ser Ala Asp
 210 215 220

Cys Val Ser Leu Thr Gly Ala Val Ser Leu Ala Ser Met Leu Thr Glu
 225 230 235 240

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Ile Phe Leu Leu Gln Gln Ala Gln Gly Met Pro Glu Pro Gly Trp Gly
245 250 255

Arg Ile Thr Asp Ser His Gln Trp Asn Thr Leu Leu Ser Leu His Asn
260 265 270

Ala Gln Phe Asp Leu Leu Gln Arg Thr Pro Glu Val Ala Arg Ser Arg
275 280 285

Ala Thr Pro Leu Leu Asp Leu Ile Lys Thr Ala Leu Thr Pro His Pro
290 295 300

Pro Gln Lys Gln Ala Tyr Gly Val Thr Leu Pro Thr Ser Val Leu Phe
305 310 315 320

Ile Ala Gly His Asp Thr Asn Leu Ala Asn Leu Gly Gly Ala Leu Glu
325 330 335

Leu Asn Trp Thr Leu Pro Gly Gln Pro Asp Asn Thr Pro Pro Gly Gly
340 345 350

Glu Leu Val Phe Glu Arg Trp Arg Arg Leu Ser Asp Asn Ser Gln Trp
355 360 365

Ile Gln Val Ser Leu Val Phe Gln Thr Leu Gln Gln Met Arg Asp Lys
370 375 380

Thr Pro Leu Ser Leu Asn Thr Pro Pro Gly Glu Val Lys Leu Thr Leu
385 390 395 400

Ala Gly Cys Glu Glu Arg Asn Ala Gln Gly Met Cys Ser Leu Ala Gly
405 410 415

Phe Thr Gln Ile Val Asn Glu Ala Arg Ile Pro Ala Cys Ser Leu Ser
420 425 430

Glu Lys Asp Glu Leu
435